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NPEYLGLDVP 1246
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| NAEYLRVAPP 1202
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 73
                           HLTGCPKCDPSCPNGSCWGRGEENCQKLTKIICAQQCSRRCRGRSPSDCCHNQCAAGCTG
                                                                                                                                                                                                                                 GCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVF
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LLAALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRN
                                                                                                                                                                                                                 PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST
                                                                                       129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR
                                                                                                                                                    S-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTG
                                                                                                                                                                                                                                                                                                                                                       361 YCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAMPENWTDLHAF
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1134 QPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TPQ
                                            1094 Q-SVPKRPAGSVQNPVYHNQPLHP-----APGRDLHYQN--PHSNAVSNPEYLNTAQ
                                                                                                                            1193 GGAAPQPHPPPAFSPAFDNLYYWDQ------DP----PERGAPPSTFKGTPTAE
                                                                                                                                                                            [1] SEQUENCE FROM N.A. SERAINCE FROM N.A. SERAINCE FROM N.A. SERAINCE STRAINCE STRAINCE STRAINCE J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J. Sarclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative genomic sequence analysis and isolation of human amouse alternative Egfr transcripts encoding truncated receptor isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1210 AA
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SMART; SM00220; S_TKc; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00107; PROTEIN KINASE_DAP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
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InterPro; IPR000494; EGFF_L domain.
InterPro; IPR000119; Euk_pkInase.
InterPro; IPR0002104; Furin-like.
InterPro; IPR002209; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Ffam; PF00057; Furin-like; 1.
Ffam; PF01030; Recep_L_domain; 2.
PRINTS; PR00109; TYRINASE.
ProDom; PR000001; Euk_pkinase; 1.
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                                                                                                                                                                                                                                                                                      -----EYVNOPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTN 1106
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                                                                                                                                                                                                                                      1122 PLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSPG
                                                                                                                                 1063 PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                              ------kykrin-rogs-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 2643.5; DB 13; Length 1137; larity 46.2%; Pred. No. 1.3e-189; Conservative 173; Mismatches 350; Indels 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99263203, PubMed=10328884;
Dixon M., Lumsden A.;
"Distribution of neuregulin-1 (nrgl) and erbB4 transcripts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1137 AA; 127927 MW; 4D616436F87DC84F CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1137 AA
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Pfam; PF00069; pkinase; 1.
Pfam; PF00109; Pkinase; 1.
Pfam; PF07257; YLD; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00261; FU; 3.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     embryonic chick hindbrain.";
MOI. Cell. Neurosci. 13:237-258(1999).
EMBL; AF121963; AAD31764.1; -.
HSSP; P11362; 1FGK.
INTERPRO; IPRO00494; EGFR L domain.
INTERPRO; IPRO00719; EUK pkinase.
INTERPRO; IPRO01719; FUX pkinase.
INTERPRO; IPRO01368; TVFR_C6.
INTERPRO; IPRO01265; TYF_Dkinase.
INTERPRO; IPRO01265; TYF_Dkinase.
INTERPRO; IPRO01265; TYF_Dkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor tyrosine kinase (Fragment)
ERBB4.
                                                        996 SDD--DVVDADEYLL-----
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1142 GMFLPAAENLEYLGL 1156
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                                                                                                                                                                                                                                                         VQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA 115
                                                                                                                                                                                                                                                                                      234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 KANSKFIGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 YISAWPDSLPDLSVFONLOVIRGRILHNGAYS-LTLOGLGISWLGLRSLRELGSGLALIH 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 VIMWWPENWISLSVFQNLEIIRGRITFSRGFSFVVVQVSHLQWLGLSSLKEVSAGNVILK 467
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                                                                                                                                                    1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
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                                                Length 1165;
1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                              tch 39.0%; Score 2646; DB 13; al Similarity 44.7%; Pred. No. 8.7e-190; 570; Conservative 163; Mismatches 388;
                                                                                                                                                                                                                                                                                                                                                               116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YPKDG--PSGLNQLGLMNLTEILDGGVQIINNKYLRYGPWYWRDII-RNNDAPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 WRLILMCVASRLRAASSQTQEAVCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEI
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                                                                                                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1328;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99177347; Pubmed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA around the wntl locus rubripes.";
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                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ErbB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.4%; Score 2262; DB 13; 39.8%; Pred. No. 7.7e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 39.8%; Pred. No. 7.7e-161;
Matches 512; Conservative 162; Mismatches 413;
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HSSP; P11562; IFCK.
HSSP; P11622; IFCK.
INTEAFDO: IPRO00194; EUK EATAGAMIN.
INTEAFDO: IPRO01794; EUK EATAGAMIN.
INTEAFDO: IPRO0174; FUTIN-11ke.
INTEAFDO: IPRO01745; FUTIN-11ke.
INTEAFDO: IPRO0175; FUTIN-11ke.
INTEAFDO: 
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YL 1114
                                      YL 1241
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                                                          221 AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF
                                                                                ESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCA
                                                                                                                                                                                                                RVCYGLGMQYIKANSKFIGITELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQ
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SEQUENCE FROM N.A.
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                                                                                                                             TCVAGCHFNSGIPREFAGLNGVCVACHPECKPQTGKASCTGPGADECMACTKFRDGPYCM
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                                                  VMWTQLFRGSRVRANSLNSNRPMAECVADGRVCDPLCSDSGCWGPGPDQCLSCRNYSRHG
                                                                                                                                                            ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA
                                                                                                                                                                      SCPAGVN-DGEKGLIFKFPNREGHCEPCHQNCTQGCSGPGLNDC---LEAARLTISSGQ
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           VPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                                                                                    ECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
BLE-FAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
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                                       PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment).
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Anopheles gambiae (African malaria mosquito).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                     Table Transport (1972)

Table 
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NON TER 1 1 159585 MW; E3D9D88967724F07 CRC64;
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DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                      Henner W.D.;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Hypothetical 40.2 kDa protein.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                        Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                   MEDIINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secreted
autoinhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 419;
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR00174; Purin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L domain; 1.
SMART; SM00261; FU; A. 45472 MW; FECIBE347E2D030C CRC64;
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.6%; Score 1871; DB 4;
Best Local Similarity 98.8%; Pred. No. 3.4e-132;
Matches 341; Conservative 1; Mismatches 3;
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(TrEMBLrel. 13, (TrEMBLrel. 16, (TrEMBLrel. 21,
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01-JUN-2002
    01-MAY-2000
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  PHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQ
                          SDHEVMVQKNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLDSCK---
                                                                                                             507 SLPRLYSVDSKTCGDCHQECKD-----FCYGPNEDNCGSCMNVKDGRFCVAECPTTKHAM
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                                                                                                                                                                                                                                                                                                 622 QEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQDFYANEE
                                                                                                                                                                                                                                                                                                                                           --ACQPCPINCT-----HSCVDL-----DD-----KGCPAEQ-----
                                                                                                                                                                                                                                                                                                                                                                      682 TRICLPCHQECRGCHGLGDDHHECRNLKLFEGDPYDNATTFTCVSNCPASHPYKRFPQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                -------RASPLTSIVSAVVGILLVVVLGVVFGILI--------QYIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                681 NSKFIGITEL-PLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
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                                                                                    GLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
    Matches 330; Conservative
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POLYPROTEIN.
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                                                                                                941 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
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                                                                                                                                                                      LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEE
                                                                 Gaps
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
Wan D.F., Gu J.R.;
"Novel human cDNA clones with function of inhibiting cancer cell
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.1%; Score 1697.5; DB 4; Length 412; 80.5%; Pred. No. 3.6e-119;
                                             Length 367;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF318349; AAL55856.1; -.
InterPro; IPR002048; EP-hand.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00069; pkinase.; I.
EMBL; BC027080; AAH27080.1; -.
Hypothetical protein.
SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44702 MW; 034397FF3F27D2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
                                          Query Match
25.7%; Score 1739; DB 11;
Best Local Similarity 88.0%; Pred. No. 2.3e-122;
Matches 323; Conservative 11; Mismatches 33;
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SMART: SM0219; TyrKC; 1.
PROSITE; PS00011; EF HAND; UNKNOWN 1.
PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.
Hypothetical protein.
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RX MEDLINE=94203659; PubMed=8152791;
RA Vennetrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
RA Johnsson A., Beug H.;
Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT "Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT cevolution of distinct viral genomes carrying mutant v-erbB genes with
different transforming capacities.";
Concogene 9:1307-1320(1994).
Concogene 9:1307-1320(1994).
CONCOGENE 9:1307-1320(1994).
CONCOGENE 9:1307-1320(1994).
CONCOGENE 9:1307-1320(1994).
CONCOGENE 9:1307-1320(1994).
CONCOGENE PROMOTO: Retro M.
CONCOGENE PROMOTO: Retro M.
CONCOGENE PROMOTO: Retro M.
CONCOGENE PROMOTO: PROTEIN KINASE ATP; 1.
CONCOGENE PROMOTO: PROTEIN KINASE ATP; 1.
CONCOGENE PROMOTO: PROTEIN KINASE TYR; 1.
CONCOGENE PROMOTO: RANSELDE TYR; 1.
CONCOGENE PROTEIN KINASE TYR; 1.
CONCOGENE TANSFERDE TYRORIEL TANSFERDE TYR; 1.
CONCOGENE TANSFERDE
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                                                         1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                               IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                                                                          61 IDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                                                                                                                                                                                                          LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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Best Local Similarity 53.1%; Pred. No. 3e-114;
Matches 346; Conservative 77; Mismatches 121; Indels 108;
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11950;
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                                                                                                                                                                                                                                                                750 NTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRL 809
                                                                                                                                                                                                                                                                                                                                                                                       175 ATSPKANKELLDEAYVWASVDNPRVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNI 234
                                                                                                                                                                                 578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                      GSQDLLMWCMQ1AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEY
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MEDLINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
"Six amino acids from the retroviral gene gag greatly enhance the transforming potential of the oncogene v-erb-B.";
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                                                                                                                                                      Indels 108;
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                                                                                                                        Length
                                                                                        567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UJV-2002 (TrEMBLrel. 21, Last annotation update)
Gag.V-erb-A, V-erb-B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian erythroblastosis virus.
Viruses, Retroid viruses, Retroviridae, Avian type
VCBI_TaxID=11861;
                                                                                                                    24.1%; Score 1635; DB 15;
53.7%; Pred. No. 2.9e-114;
tive 75; Mismatches 115;
FRUSITE; PS50011; PROTEIN KINASE DOM; 1. PROSITE; PS00109; PROTEIN KINASE TYR; 1. Tyrosine-protein kinase.
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                                                                                                                                       Best Local Similarity
                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                   495 SEISSVLEKGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLV 554
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                                                                                                                                                                                                                                                             LLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPA 920
                                                                                                                                                                                                                                                                                                                       REIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVV 980
                           141 PEETATPKTGP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHP 197
                                                                          PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLD 800
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94203659; PubMed=8152791;
MEDLINE=94203659; PubMed=8152791;
Wennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genee with
different transforming capacities.";
Oncogene 9:1307-1320(1994).
                                                        NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILI--QYI---KANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          599 NSPST-----RNGÖGHÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 VREDSFVQRYSSDPTGNFLEESIDDGFL-----PAPEYVNQ--LMPKKPS-----
                                                                                                                     KFIGITEL -- PLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKI
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Viruses, Retroid viruses, Retroviridae, Alpharetrovirus.
VCBI_TaxID=11950;
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InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; FS00107; PROTEIN_KINASE_ATP; 1.
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ò 541 VEBÇRVLOGI, PRE, YVNAR, HCLP.------GPPECQ 568 354 :|-; IEKCQESYLLAFEHYINYRKHNIPHFWSKLLMKVADLRMIGAYHASRFLHMKVECPTELS 413 569 PONGSVTCFGPEADOCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEGACOPCPI 628 414 PQE-----VGP---DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VMKYADANAVCOLCHP 465 629 NCTHSCVDLDDKGCPAEORASPLTSIVSAVV-GILLVVVLGVVFGILI--OYI---KANS 682 466 NCTRGCKGPGLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRHHVRKRTLR 522 683 KPIGITEL--PĻTPSGAMPŅOAOMRILKĒTELRKVKVLGSGAFGTVYKGINIPDĢENVKJ 740 523 RLLOERELVEPLTPSGEAPNOAHLRILKETEPKKVKVLGFGAFGTVYKGLWIPEGEKVTI 582 Query Match Best Local Similarity 23.2%; Score 1570.5; DB 15; Length 962; Matches 346; Conservative 75; Mismatches 145; Indels 125; Gaps 741 PVAIKVLKENTSPKANKEILDEAYVMAGYGSPYVSRLLGICLTSTVQLVTQLMPYGGLLD 800 583 PVAIKELREATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITOLMFYGCLLD 642 801 HVRENRGRLGSODLLINWÇMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLAR 860 643 YIREHKDNIGSOYLLINWCVOIAKGMOYLEERHWVHRDLAARNVLVKTPQHVKITDFGLAK 702 861 LLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPA 920 921 REJPOLLEKGERLPOPPICTÍDVYMÍNVKCÝMIDSECRPRFRELVSEFSRMARDPORFVV 980 763 SEISSYLEKGERLPQPPICTIDVYMIMVKCMMSGADSRPKFRELIAEFSKMARDFRYYLV 822 981 jo-nedlgpaspldstfyrsilledddmgplydaesylypogoffcpdpargagmyhhrh 1039 1040 RȘSSȚRSGGDLTLGLEPSEEAPRSPLAPȘEGAGȘDVPDGDLGMGAAKGLQSLPTHDPS 1099 867 NSPST------SRTPLLSSLSATSN-----NSATKCIDRNGGH--- 898 අ ò ΩP ठे PP

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4 2 F 1000000 mg.	OF SUPERIOR SCHOOL OF THE SCHURDSHAFT. OF SUPERIOR MANAGE SCHURDSHAFT. Numerical Substitution of Schurdshaft. OF SUPERIOR SUPERIOR SCHURDSHAFT. RAME STRANGESTEL/61; From the Human and Mouse EGFR Genee Encode STRANGESTEL/61; From the Human and Mouse EGFR Genee Encode STRANGESTEL/61; From the Human and Mouse EGFR Genee Encode STRANGESTEL/61; From the Human and Mouse EGFR Genee Encode STRANGESTEL/61; From the Human and Mouse EGFR Genee Encode STRANGESTEL/61; From the Human and Mouse EGFR Genee Encode STRANGESTEL/61; From the FROM N. A. LEARNING SCHURDSHAFT. [2] DENCE FROM N. A. 129/SVJ, AND 129/SVJTAC; SCHURK K. E. Danielsen A. J. R. Submitted (JAN-129/S). RAME SEQUENCE FROM N. A. 129/SVJTAC; SCHURK K. E. James C. D. R. STRANGESTEL/61; Page 181 N. S. Geen P. J. Yee D. James C. D. S. Page 181 N. S. Gene FROM N. S. GENE STRANGESTEL/61; Page 181 N. S. Gene P. James C. D. N. R. SHARMINE S. GENE STRANGESTEL/61; Page 181 N. S. GENE STRANGESTEL/61; Page 18

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July 22, 2003, 08:41:54; Search time 36.6984 Seconds (without alignments) 4527.811 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                       1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1247
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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6776
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human herequlin 2	Human tyrosine kin	HER2 transgene pla	Human HER2 (ErbB2)	HER-2/neu protein.	Human HER-2/neu on	Human HER-2/neu pr	Amino acid sequenc	Human HER-2/neu pr	HER2/neu amino aci
SUMMARIES			ID		AAE12130	AAB60167	AAU74545	AAWO1111	AAW92406	AAB21198	AAY84780	AAB85458	AAG88267
			DB	21	22	22	23	17	20	21	21	22	22
			e Match Length DB 1	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
	مين	Query	Match	97.5	97.5	97.5	97.5	97.4	97.4	97.4	97.4	97.4	97.4
			Score	8099	6608	6608	6608	6602	6602	6602	6602	6602	6602
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Human Her-2 protei	Her-2/		Human Her-2/neu po	Sequence of c-erbB	Human breast cance	Human HER-2/neu pr	Rat HER-2/neu prot	Rat Her-2/neu onco	Mouse Her-2/neu pr	acid seque	Mouse Her-2/neu on	Human HER-2/neu fu	Her-2/neu extracel	Mouse Her-2/neu ex	Mouse Her-2/neu ex	Human HER-2/neu fu	u	Her2-GM-CSF immuno	Extracellular HER-	Human Her-2/neu on	Human ErbB2 oncopr	Human ErbB2 extrac	DC8scFv-erbB2EC fu	Extracellular port	Amino acid sequenc	Human EGF receptor	Human Her-1 protei	Human epidermal gr	Amino acid sequenc	Rat HER-2/neu_prot	Rat Her-2/neu onco	Human epidermal gr	Human protein for	
AAE24067	AAE20479	AAM51143	AAU77114	AAR39568	AAU98923	AAB21208	AAB21199	AAM51144	AAB21206	AAG62860	AAM51151	AAB21203	AAM51148	AAM51152	AAM51153	AAB21204	AAM51149	AAW19764	AAB21200	AAM51145	AAB60408	AAB61593	AAY44993	AAR08222	AAB19259	AAY50616	AAE23019	AAM50768	AAB68420	AAB21205	AAM51150	ABP51768	AAE20483	AAE20481
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ALIGNMENTS

T 1 620 AAY92620 standard; Protein; 1255 AA. AAY92620;	10-AUG-2000 (first entry)	Human heregulin 2 (Her2).	Heregulin 2; Herz; vaccination; cytotoxic T-lymphocyte immunity;	cell-associated peptide antigen; foreign epitope.	Homo sapiens.	ey Location/Qualifiers	Domain 1173		/Note= "mature polypeptide" Region 525	/note= "suitable for foreign epitope insertion"	/label= insertion	/note= "suitable for foreign epitope insertion" Region 103117	/label= insertion region /label= insertion"	
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with ceancars (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her3) and/or fibroblast growth factor 8b (FGF8B). The method comprises effecting simultaneous presentation by antigen producing cells (APCB) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the FA and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGPBb comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
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                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 6608; DB 21; Length 1255; 97.4%; Pred. No. 0; ive 8; Mismatches 17; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 97.4
Matches 1222; Conservative
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655.1010
/label= Tyrosine_kinase_uc...
661.675
/label= insertion region
/note= "suitable for foreign epitope insertion"
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|note= "suitable For foreign epitope insertion"
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'note= "suitable for foreign epitope insertion"
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/label= insertion region
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YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                          LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                                                                    HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1247
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                                                                                                                                                                                                 transcripts that are expressed in antigen presenting cells (APCS), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide (774-782).
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Claim 4; Page 63-67; 69pp; English
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and pl85nsu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP
                                         YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating tumors, particularly breast cancers, which overexpress an receptor and does not respond to an anti-ErbB antibody, comprises conjugating the antibody to a maytansinoid -
                                                                                                                                                                                                                                                                                                                                                          GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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16-MAR-2000; 2000US-0189844.
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is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endomerrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                    The invention relates to treating a tumour in a mammal, where the tumour
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841 LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                   EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                            HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                       HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                   IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                            EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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05-OCT-2000; 2000US-238327P.
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(SCHW/) SCHWALL R.
(SLIW/) SLIWKOWSKI N
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               Human HER-2/neu protein (AAM01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overing, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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9; Mismatches
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Best Local Similarity 97.2%;
Matches 1220; Conservative 9
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      LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWALESILRRRFT
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for treating or
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                                                                                                                                                                                                                                                                                       oncogene; immune response; T cell; B; treatment; tumour.
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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tummour, or to prevent tummour occurrence or reoccurrence.
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                                                                         IDSECRPRERELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                         EEYLVPQQGFFCPDPAPGAGGWVHRHRSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                                                                                   AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                                                                                         NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
             IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                           EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                                                                    AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                                                                          NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                                                                                                                                                               HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                AAB21198 standard; protein; 1255 AA
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                                              EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                   NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                                                                                                              The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as archropathy, bone resorption, inflammatory diseases, degenerative disorders of the
                                                                                                                                                                                                                             GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1247
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central nervous system and wound healing
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erbB-2, inhibitors of
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                                                                                 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                              ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                                     DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                                                                                             AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                   expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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                                                  AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                    NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes isolated prepared HERATone epitopes (1). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (II) bund to a culture in vitro and binds to a complex of an epitope (II) bund to a culture in vitro and binds to a complex of an epitope (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino cids that have 100% identity with a native peptide sequence of HERATONE, (3) a vaccine composition (III) comprising (II) and a pharmaceutical corposition (III) comprising (II) and a pharmaceutical corposition (III) comprising (II) and substance composition (III) comprising (II) and substance and cardendard ancleic acid encoding a peptide comprising (II); and (II) are useful for and immunostimulant activities, and can be used in vaccines (I), (II) cand (III) are useful for and immunostimulant activities, and can be used in vaccines (I), (II) cand (III) are useful for and immunostimulant activities, and can be used in vaccines for the prevention and treatment of cancer. (I) and (II) are useful for antigen when incubated with a T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present complement of the present of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes and effects caused by infectious agents or whole protein antigen is eliminated. The vaccine sprovides the ability to direct and focus an immune response to multiple tumour-associated molecules addressing the problem of tumour cultumour-associated molecules addressing the problem of tumour escape due to antigen loss. And88266 to AAG89121 represent amino acid sequences used in the exemplification of the present invention.
NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
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cancer -
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                                                                                                                                                                                                                                                                             Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                               An isolated prepared HER2/neu epitope useful in a vaccine for cellular immune responses for the prevention and treatment of
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                                                                                                                                                 standard; Protein; 1255
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                                         1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                       MELAALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHI.DMLRHLYOGCOVVOGNL
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AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV 1132
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              ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                    DPLNNTTPVTGASPGGLRELQLRSLTBILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                    LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
                                      NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                         1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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Pred. No. 0;
9; Mismatches 18;
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Best Local Similarity 97.2%;
Matches 1220; Conservative 9
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N-PSDB; AAD38904.
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Location/Qualifiers
1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
                                                                                                                                                                                                                       Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                      GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1247
                                                 Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
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21-FEB-2001; 2001US-270520P
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Mcneill PD, Vedvick
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Query Match

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                                                                   NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                               GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1247
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tyrosine kinase; receptor; c-erbB2; gene therapy.
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comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated concert, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu concertion protein and patient. T cells that specifically react with a Her-2/neu concertion protein and patient. T cells that specifically react with a Her-2/neu concertion protein can be used to remove tumour cells from a sample in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ELTYLPTNASLSFLQDIQEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     order to inhibit the development of cancer in a patient
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Zhneu or a polynucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic lympkowa. I hoss myelomas hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-Zhneu polypeptide.
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                                                                                                                                                               LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                               IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Her-2/neu; cytostatic; haematological malignancy; CML;
acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLI
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
                                                LVHRDLAARNVLVKSPNHVKITDFGLARLLDI
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                           EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                                                  AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                                                                           NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
                                                                IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                    EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                                                                               etc.
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No. 0;
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Pred.
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Best Local Similarity
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Search completed: July 22, 2003, 09:16:33 Job time : 41.6984 secs

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(without alignments)
4403.399 Million cell updates/sec
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.: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Human herequily	Human tyrosine kin	HER2 transcene ola	Human HER2 (ErhB2)	HER-2/new protein	Human HER-2/neu on	Human HER-2/neu or	Amino acid semena	Human HER-2/neu or	HER2/neu amino aci
SUMMAKIES		ΙD	AAY92620	AAE12130	AAB60167	AAU74545	AAW01111	AAW92406	AAB21198	AAY84.780	AAB85458	AAG88267
		DB	21	22	22	23	11	20	21	21	22	22
		e Match Length DB	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
ď	Query	Match	97.9	97.9	97.9	97.9	97.8	97.8	97.8	97.8	97.8	97.8
		Score	6657	6657	6657	6657	6651	6651	6651	6651	6651	6651
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Human Her-2 protei Human Her-2/neu pr Human Her-2/neu on Human Her-2/neu bo Sequence of c-erbB Human breast cance Human HER-2/neu prot Rat HER-2/neu prot Rat HER-2/neu prot Rat HER-2/neu on Mouse Her-2/neu on Human HER-2/neu ex Her-2/neu extracel Mouse Her-2/neu ex Human HER-2/neu ex	Human Her-2/neu on Human ErbB2 oncopr Human ErbB2 extrac DCBscFv-erbB2EC fu Extracellular port Amino acid sequenc Human Her-1 protei Human protein for Human epidermal gr
AAE2406 AAE2047 AAU77114 AAU77114 AAR3956 AAR3195 AAB2119 AAB2119 AAB2120 AAB2120 AAB2120 AAM5114 AAM5115 AAM5115 AAM5115 AAM5115 AAM5115 AAM5115 AAM5115 AAM5115 AAM5116	AAM51145 AAB60408 AAB601593 AAY44993 AAX08222 AAX08222 AAX05016 AAX23019 AAX2016 AAX2016 AAX20483 AAX20483 AAX20481 AAX20481 AAX20481
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620 AAY92620 standard; Protein; 1255 AA.	(620)		10-AUG-2000 (first entry)		Human heregulin 2 (Her2).	•	Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunit	self-protein; cancer; breast cancer; prostate cancer;	cell-associated peptide antigen; foreign epitope.		sapiens.	•	Location/Oualifiers		/label= N-terminal	/note≈ "mature polypeptide"		/label= insertion region			/label= insertion_region			/label= insertion_region			/label= insertion_region		11 1.4323
F .Y92620 ID AAY92	AAY92620:		10-AU		Human		Hereg	self-	cell-		Ношо		Key	Domain			Region			Region			Region			Region		, e a	DOI:10
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T helper epitopes were identified (see features table). The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor associated
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| Jabel= insertion region
| note= "suitable for foreign epitope insertion"
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/label= insertion region
/note= "guitable For foreign epitope insertion"
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Birk P, Karlsson G;
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/label= Tyrosine_kinase_domain
                                                                                         /label= Ligand_binding_domain
 'label= Cysteine_rich_domain
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98US-0105011.
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                               cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 Escal group derived from the cell-associated PA, and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epicopes of the respective PA and including at least to efforcing T helper epitope are also claimed. The method is used to treat prostately prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DPLMNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex. (WHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as compounds of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen. HBR-2. Polynucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present confirm transduction of polynucleotides into host cells. The present confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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       IDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                                                                                                                                                                conjugate; cancer;
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is characterised by the overexpression of an epidermal growth factor receptor (BrbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, compirising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating energy, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ovan stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; immorphagal disorder; inflammatory disorder; angiogenic disorder; inflammatory disorder;
                                                                                                  IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                  HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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          Human HER-2/neu protein (AAM01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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676.1253
//Abble Intracellular domain
/note= "claimed domain, useful for immunisation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2/neu; c-erbBl; p185; oncogene; tyrosine protein kinase; breast cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
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of this protein is used in a method for eliciting or enhancing an immune response to HER.2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER.2/neu protein. The method can be used for immunisation against a malignancy in which the HER.2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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HQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYM1MVKCWM
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(SMIK ) SMITHKLINE BEECHAM.
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                                                                                                                                                      NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                                                          The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be used to detect SPLICE erbB-2 in a sample. Agents SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the
                                            EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                                                                                               Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
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                                                                                                AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is

Culture in vitro and binds to a complex of an epitope (I), bound to a

chuman leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

acids that have 100% identity with a native peptide sequence of HER2/neu;

(3) a vaccine composition (III) comprising (II) and a pharmaceutical

excipient; (4) an isolated nucleic acid encoding a peptide comprising

(I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic

and immunostimulant activities, and can be used in vaccines. (I), (II)

and (III) are useful for inducing callular immune responses for the

prevention and treatment of cancer. (I) and (III) are useful for

and immunostimity and immune response to a tumour-associated

antigen when incubated with a T lymphocyte sample form a patient and

detecting the presence of bound T lymphocyte sample form a patient and

detecting the presence of bound T lymphocyte sample form a patient con

conditions mean that immunosuppressive epitopes that may be present

in whole antigens may be avoided. Selected epitopes and be organed by

infectious agents or whole protein antigen is eliminated. The vaccine

provides the ability to direct and focus an immune response to multiple

conditions and the opportunity to combine epitopes aderived from

which is an examinated antigens from the same pathogen. Epitope and

contigen loss. And8s266 to AAG89121 represent amino acid sequences used in

the exemplification of the present invention.
1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
                                                                                                                                                                                                                                                             Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer -
                                            GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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EEYLVPQQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                          AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothicate backbone.
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Matches 1225; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for celiciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.

The composition is useful for the therapy and diagnosis of cancer.

The compositions for the diagnosis, prevention and treatment of and other compositions for the diagnosis, prevention and treatment of cancer in a chuman malignancies, for stimulating and/or expanding T cells specific for human malignancies, for stimulating and/or expanding T cells specific for ther-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating art cell response in a chuman patient, as probe or primer for nucleic acid hybridisation, to callering the centire Her-2/Neu gene or gene fragments of interset, to isolate a full centire Her-2/Neu gene readments of interset, to isolate a full centire Her-2/Neu gene in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-second sequence is human Her-2/Neu protein.
Human, Her-2/Neu protein, immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope"
                                                      GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                                                                         /note= "Naturally processed HLA-B44-restricted
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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                                                                        EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of human Her-2/neu (p185 glycoprotein or C-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplifted and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines
                                NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                      GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                                  Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185; tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                            Human Her-2/neu oncogene-encoded p185 glycoprotein.
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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comprising the fusion proteins or nucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated concern specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostete cancer in a patient. T cells that specifically react with a Her-2/neu colon, fusion protein can be used to remove tumour cells from a sample in
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IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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Page 71-74; 74pp; English.

Disclosure;

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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polymetlectide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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Search completed: July 22, 2003, 08:41:45 Job time: 42.9774 secs

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July 22, 2003, 08:22:34; Search time 48.3575 Seconds (without alignments) 5347.444 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O18735 canis famil	O90x70 rattus norv	O9ep98 mus musculu	O9vh40 xinhonhorus	Ogweff callus call	P79754 fuon mibrin	O9bih9 anopheles	Oguk79 homo sanien	OBr2x1 mis miscilli	O8wvv0 homo sapien	086712 avian rous-	086714 avian roug-	O64895 avian ervth	O85468 avian ervth	Other Family mischilling	
SUMMARIES	ΙD	018735	05X70	Q9EP98	Q9YH40	O9W6F6	P79754	641860	Q9UK79	08R2X1	QBWYVO	086712	086714	064895	085468	O9WVF5	Q9ERV6
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Q9y1x8 ephydatia f		Q26566 schistosoma	Q90836 gallus gall	Q9ese0 rattus norv	Q9psh2 gallus gall	Q14256 homo sapien	Q923v5 rattus norv	. P11776 xiphophorus	Q8szwl drosophila	Q99162 xiphophorus	Q9bud7 homo sapien	Q9pvz4 xenopus lae	Q9njv5 biomphalari	Q9bg66 oryctolagus	093457 scophthalmu	Q8uw85 paralichthy	Q8uw86 paralichthy	Q9u5a8 bombyx mori	073798 xenopus lae	Q8uw84 paralichthy	Q8uw83 paralichthy	Q9ygh8 scophthalmu	Q9vd94 drosophila	Q9qvw4 rattus sp.	O91ym0 mus musculu	O96135 homo sapien		Q07912 homo sapien
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ALIGNMENTS

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"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990).
AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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Eukaryota; Metazoa (Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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R INTERPRO; 1PR000419; EUK DKInase.
R INTERPRO; 1PR0001719; EUK DKInase.
R INTERPRO; 1PR001245; TYL DKINASE.
R PEam; PF00069; DKINASE; 1.
R PFam; PF00069; DKINASE; 1.
R PFAM; PF00069; TYRKINASE.
R PRODOM; DR00001; EUK DKINASE.
R PRODOM; DF00001; EUK DKINASE.
R PRODOM; PR0111; PR07111; SWART; SW00219; TYRK; 1.
R PROSITE; PS00110; PR07111 KINASE ATP; 1.
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MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee
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STRAIN=FISHER; TISSUE=LIVER;
Guttridge K., Dawson T.L., Earp H.S.;
Submitred (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M37394; ARP14008.1; -
HSSP; P11362; 1FGK.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Eggramal growth factor receptor.
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Matches 639; Conserv
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                                                   MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                           Gaps
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  Query Match 90.4%; Score 6147; D
Best Local Similarity 90.0%; Pred. No. 0;
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1134 SPQPEYVNOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN 1193
                                                                                             PEYLNTAQ-----PTCLSSGPDSSALWIQKGSHQMSLDNPDYQQDFFPKEAKPNGI 1185
                                ------DP-----PERGAPPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schell C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Mainle N.J.,
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C3H/101, 129/SVUJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.,
                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative genomic sequence analysis and isolation of human and uses alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative genomic sequence analysis and isolation of human amouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF275366; AAG28045.1; -.
EMBL, AF275364; AAG28045.1; JOINED.
EMBL, AF275365; AAG28045.1; JOINED.
EMBL, AF275365; AAG28045.1; JOINED.
EMBL, AF275367; AAG28045.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOST; TILSO21 IFGK.

MOST; S2244, BGERL.

INTERPRO; IPR000345; CYtC_heme_bind.

INTERPRO; IPR000494; CYtC_heme_bind.

INTERPRO; IPR000174; FURTh.Ide.

INTERPRO; IPR002174; FURTh.Ide.

INTERPRO; IPR002174; FURTh.Ide.

INTERPRO; IPR002174; FURTh.Ide.

INTERPRO; IPR002174; FURTh.Ide; I.

Pfam; PF00107; Ritin-like; I.

Pfam; PF010107; Recept_domain; 2.

PROMITS; PR00109; TYRKINASE.

INTERPROSELIFU; S. TKC; I.

SMART; SM00221; FU; S. TKC; I.

PROSITE; PS001107; PROTEIN KINASE ATP; I.

PROSITE; PS001107; PROTEIN KINASE DOM; I.

PROSITE; PS001107; PROTEIN KINASE DOM; I.

PROSITE; PS001107; PROTEIN KINASE TYR; I.
                                                                                                                                                                                                                     1210 AA
                                                                    PEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-
                                                                                                                       FKGTPTAENPEYLGLDVP 1254
                                                                                                                                                 FKG-PTAENAEYLRVAPP 1202
                                                                                                                                                                                                                            Q9EP98;
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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|KCWMIDADSRPKFRELILEFSKWARDPQRYLVIQGDERMHLPSPTDSNFYRALMEEEDME 1009
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                                                                                          239
                                                                                                                                                                                  CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTVNTDTFESMPNPEGRYTFGASCVTAC 299
                                                    124
                                                                           PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL 181
                                                                                                                                                                                                                                      PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQY1KANSKFIGI 359
                                                                                                                                                                                                                                                     LPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVH 478
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                                       LAALCAAG------GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
                                                                                                                              TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ
                                                                                                                                              LTYLPTNASLSFLQDIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
                                                                                                                                                                                                 TELE-FAGCKKI FGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWPDS
                                                                                                                                                                                                                                                                                                                                                                                                     TVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 TCPSGIMGENNTL-VWKFADANNVCHLCHANCTYGCAGPGLKGC--QQPEGPKIPSIATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVGILLVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
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GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS 1235
                  1010 EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
                                                                                                                ---EPCIPPNGH------PVRENSIALRYISDPTQNALEKDLDGH- 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC 220
                                                                                                                                                                    -----RYKRIN-RQGS------
                                                                                 1070 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
                                                                                                                                                1129 APLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=992652303; PubMed=10328884;
MEDLINE=992652303; PubMed=10328884;
Dixon M., Lumsden A.;
"Dixon M., Lumsden A.;
"Dixon M., Lumsden A.;
"Dixon M., Lumsden A.;
"Dixon Molonic chick hindbrain.";
Mol. Cell. Neurosci. 13:237-258(1999).
EMBL; AF121963; ARD31764.1; --
HSSP; P11362; 1FGK.
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                                                                                                                                                                                                                                                                                                                                                                                                Q9W6F6 PRELIMINARY; PRT; 1137 AA. Q9W6F6; Q1NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-2099 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Receptor tyrosine kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SWART; SM00261; FU; 3.
SWART; SM00219; TYPKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
RNOSITE; PS00652; TNFR NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000494; EGFR L domain.
InterPro; IPR001019; Euk pkinase.
InterPro; IPR001019; Furin-like.
InterPro; IPR001018; TNFR c6.
InterPro; IPR001045; TVF pkinase.
InterPro; IPR001045; TVF pkinase.
InterPro; IPR001045; TVF pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PP00069; pkinase; 1.
Pfam; PP01030; Recep L domain; 1.
Pfam; PP01030; Recep L domain; 1.
                                                 SSDD--DVVDADEYLL-----
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                                                                                                                                                          116 VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK 175
                                                                                                                                                                                                                                               234
                                                                                                                                                                                                                                                                                                                CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 294
                                                                                                                                                                                                                                                                                                                                                                             CCNEHCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAA 293
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                                                                  Gaps
                                                                148;
                              Length 1165;
                                                              Indels
1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                           Query Match 39.7%; Score 2698; DB 13; Best Local Similarity 45.4%; Pred. No. 5.8e-195; Matches 579; Conservative 164; Mismatches 385;
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SEQUENCE
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ebb3.
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei;
Tetraodontidae, Takifugu.
NCBI TaxID=31033;
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MEDLINE=9917347; Pubmed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
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Anopheles.
NCBI_TaxID=7165;
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                                                                                                                                    638
                                                                                                                                                                                         711 QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE 770
                                                                                                                                                                                                   HARILKPSDLRKIKPLGSGVFGTVSKGFWIPEGETVKIPVAIKTIQDSSGRQTFTEITDH 757
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                                                                                                                                                                                                                                                                                         877
                                                                                                              ARCPOYIKANSKFIGITELPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA 657
                                   VPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                                          ECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
                                                                                                                         771 AYYMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
 PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
                                               523 TCVAGCHFNSGIPREFAGLNGVCVACHPECKPQTGKASCTGPGADECMACTKFRDGPYCM
           VVGILLVVVLGVVF-----GILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
                                                                                                                                                                                                                                         LESMGSLDHPYIVRLIGICPGTCLQLVTQLSSHGSLLEHIRQHKTSLDPQRLLNWCVQIA
                                                                                                                                                                                                                                                                             1071 PRSPLAPSEGAGSDVFDGDLGMG---AAKGLQSLPTHDPSPLQ------RYSEDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GLGDRFATPSLQPSPSWSTSPSQINSYMVMTQLRYD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1118 VPLPSETDGYVAPLTCSPQP-EYVNQ-------PDVRPQPPSPREGPL--PAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GLLEADLEEDEEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --FAVSQGGHIGYLPMSPSPVDTIRQLWYQRSRLSSVRTLPDRSAFRRSSREAELCEDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BIH9 PRELIMINARY; PRT; 1433 AA.
Q9BIH9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2002 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment)
EGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YYWDQDPPERGAPPSTFKGTPTAENPE 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKMPQNSE-----CVPCKGVCPKTCPGEGI----VHSDNIG----NYKDCTIIEGSLEIL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||| : | : | | | : | : | | | : | | | : | | | DQSFDGFQOVYTNFSFGPRYIKIDPDRLEVFSTVKEITGFINIQAHHPNFTTLNYFRNLE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ISLYDLPQVILPRLQIIRGRTTFKLNKWEEAYGLFV-----SFSHMNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLRSLTEILKGGVLIQRNPQLCYQDTILWKDI-FHKNNQLALTLIDTNRSRACHPCSPMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 FYDDGVCKQECPPMQIYNPTNYFWEPNPDGKYAYGATCVRKCP-EHLLKDNGACVRKCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 PESFDGDPASNT-----APLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
Lycett G.J.;
"Cloning, expression and localisation of the Anopheles gepidermal growth factor receptor.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ301655; CAC35008.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
29.8%; Score 2028.5; DB 5;
Best Local Similarity 32.6%; Pred. No. 3.5e-144;
Matches 472; Conservative 198; Mismatches 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO0261; FU; 7.
SMART; SMO0220; S.TKC; 1.
SMART; SMO0219; TYKC; 1.
PROSITE; PSO0190; CYTOCHROME C; UNKNOWN 4.
PROSITE; PSO0107; PROTEIN KINASE ATP; 1.
PROSITE; PSO0109; PROTEIN KINASE DOM; 1.
Receptor.
NON TER.
                                                                                                                                                  InterPro; IPR000494; CytC heme bind.
InterPro; IPR000494; BGFR L domain.
InterPro; IPR000494; BGFR L domain.
InterPro; IPR002104; But Fitnase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_Kinase.
Pfam; PF001057; Furin-like; 1.
Pfam; PF00109; pkinase; 1.
Pfam; PF01030; Rece_L domain; 2.
PRINTS; PR00109; TYRKINASE.
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AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                     SEQUENCE FROM N.A.

Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AT177761; AAD56009.2; ...
InterPro; IPR000494; EGFR L domain.

InterPro; IPR002174; Furin-Iike.

Pfam; PF01030; Recep L_domain; 1.

SMART; SM00261; FU; I.

SMART; SM00261; FU; I.

SEQUENCE 419 AA; 45472 MW; FECIBE347E2D030C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kba protein.
Hypothetical (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                [1] _
SEQUENCE FROM N.A.
MEDLINEs_99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secreted
                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                     Length 419;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027080; AAH27080.1; -.
Hypothetical protein.
SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874 (1999)
                                                                                                                                                                                                                                                                                                                     Query Match 27.5%; Score 1871; DB 4; Best Local Similarity 98.8%; Pred. No. 4.5e-133; Matches 341; Conservative 1; Mismatches 3;
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            sapiens (Human)
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                                                                                                                                  autoinhibitor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGG 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1190 AVENPEYL------TPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MI------PGDKFMRLPSYTNQDEKDLIRTLAPVAMAAAAAAAAAAGASNVDVPSTIA 1152
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               NGTCINCHKTCVGCRGPRDTIAPDGCISCDKAIIGSDAKIERCLMKDESCPDGYYSDYVL
                                                                                                                                622 QEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQDFYANEE
                                                                                                                                                           --ACQPCPINCT-----HSCVDL-----DD-----KGCPAEQ-----
                                                                                                                                                                                                                                                                    688 RRLLOETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
 GLPREY-VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP-
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Last annotation update)
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(TrEMBLrel. 21, I
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PTHQHSQ 1287
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Q9UK79;
01-MAY-2000
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01-JUN-2002
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                                                                                            EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                          241 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFG
           MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                       LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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MEDLINE=94203659; PubMed=8152791;
Wennetrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Baug H.;
Johnsson A., Baug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes with different transforming capacities.";
Oncogene 9:1307-1320(1994).

EMBL: S69372; AAGG0725.1;
HSSP: P03322; LAGS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
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Pfam; PP02813; Retro M; 1.
Probom, PD000001; Buk_Dkinase; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00119; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914EFEID63 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAVENPEYLTPQGGAAPQP-----
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InterPro; IPR004028; Retro M.
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POLYPROTEIN.
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                                                                                                                                                                                                                                                                                                                           LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEE 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                     EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APLICSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG 1188
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                                                                                                                                        889 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. And D.P., Jiang H.Q., Qin W.X., Zhao X.T., Wan D.F., Gu J.R.; Man D.F., Gu J.R.; "Novel human cDNA clones with function of inhibiting cancer cell
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     Length 367;
                                                       33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
        DB 11;
Ouery Match 25.6%; Score 1739; DB 11; Best Local Similarity 88.0%; Pred. No. 3.6e-123; Matches 323; Conservative 11; Mismatches 33;
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969 113 756 173 816

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1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
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                                                                                                                                                                                               638 DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
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the
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag, V-erb-A, V-erb-B protein.
Gag, V-erb-A, V-ERB-B.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
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-!- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; X52209; CAA36459.1; --
                                                                          Indels 102;
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                                     Length 567;
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C6D9CBA7ADF725E1 CRC64;
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, Pred. No. 4.9e-119;
73; Mismatches 116;
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63390 MW;
                                   Query Match
Best Local Similarity 54.8%;
Matches 353; Conservative 7.
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567 AA;
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NCTRGCKGPGLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTL 253
                                                          DHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLA
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxID=11950;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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InterPro; IPR001245; Tyr_pkinase.
Pfam; PF0069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000010; Euk_pkinase; I.
SMART; SMO0219; TYRK; I.
PROSITE; PS00107; PROTEIN_KINASE ATP; I.
PROSITE; PS00101; PROTEIN_KINASE_DOM; I.
Tyrosine-protein kinase.
I. I.
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R PRINTS; PR00105; ZTROLDEINGER.

R PRINTS; PR00101; EUK_DKINGER.

R ProDom; PD000011; EUK_DKINGER.

R SMART; SM00130; ADLI: 1.

R SMART; SM00130; ADLI: 1.

R SMART; SM00130; ADLI: 1.

R PROSITE; PS00101; NÜCLEAR_RECEPTOR; 1.

R PROSITE; PS00101; PROTEIN KINASE DOR; 1.

R PROSITE; PS00109; PROTEIN KINASE DOR; 1.

R PROSITE; PS00109; PROTEIN KINASE DOR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

M ATP-binding; DNA-binding; Nuclear protein; Receptor;

Transcription regulation; Transferase; Tyrosine-protein kinase;

SEQUENCE 962 AA; 108320 MW; 3CSAED791E4E95CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.9%; Score 1623.5; DB 15
Best Local Similarity 51.2%; Pred. No. 8.2e-114;
Matches 354; Conservative 73; Mismatches 146;
                                 InterPro; IPR000719; Buk pkinase.
InterPro; IPR000719; Buk pkinase.
InterPro; IPR001723; Btdhrmn_receptor.
InterPro; IPR001425; Tyr pkinase.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; pkinase; 1.
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                     P10828; 2NLL.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-88217326; PubMed=2897102;
Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J., Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J., Common site of mutation in the erbB gene of avian erythroblastosis virus mutants that are temperature sensitive for transformation."; Oncogene Res. 1:265-278(1987).
EMBL; X06943; CAA30024.1; ---
EMBL; X06943; CAA30024.1; ---
HSSP; P11862; 1FGK
InterPro; IPR001245; FUL pkinase.
InterPro; IPR001245; Tyr pkinase.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retroid virusee; Retroviridae; Avian type C
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1197
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1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
                                                                                     1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maihle N.J.;
"Alternative Transcripts from the Human and Mouse EGFR Genes Encode Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              1170 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
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STRAIN=C57BL/6J; TISSUE=LIVER;
MEDLINE=21085660; Pubmed=11217851;
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44.2%; Pred. No. 4.3e-103;
ive 94; Mismatches 238; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 AA; 72906 MW; 6B34063B1BC928CB CRC64;
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EMBL, AR275365, AGC28047.1; JOINED. EMBL, AR04944; BAB23669.1; JOINED. EMBL, AK004944; BAB23689.1; BMBL, AK004911; BAB23662.1; MGD; MGT:95294; EGFR L domain. InterPro; IPR00494; EGFR L domain. InterPro; IPR00494; FGFR L domain. Pfam; PF00130; Recep L domain; 2. SMRRT; SW00261; FU; 3.
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Job time : 53.3575 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2003, 08:12:49; Search time 10.2304 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

Title: Perfect score:

SEQ4-579-593-12 6803 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	ption
	6651	97.8	1255	-	ERB2 HUMAN	P04626	homo annien
7	5862	86.2	_	-	t	P06494	raffile nors
e	5846.5	85.9	1254	-		060552	motoria note:
4	3114	45.8	1210	-	EGFR HIMAN	00000	homo garden
Ŋ	3090	45.4	121	-	EGFR_MOUSE	001279	יינייספייש פווש
9	2956.5	43.5	7			015303	
7	2944	43.3	1308		ERB4 RAT	062956	rattı
80	2657.5	39.1	1167	~	XMRK XIPMA	P13388	
9	2397.5	35.2	1342	-	ERB3 HUMAN	P21860	
10	2327.5	•	_	-	ERB3 RAT	062799	rattus norv
11		28.6	1426	-	EGFR_DROME	P04412	drosophila
12	1719.5	٠		-	ERBB_ALV	P00534	avian leuko
13	1688	٠		-	ERBB_AVIER	P00535	avian ervth
14	1600			-	ERBB_AVIEU	P11273	
15	1565			-	EGFR_CHICK	P13387	gallus gall
16	~	•	_	-	LT23_CAEEL	P24348	caenorhabdi
17	1142.5	•		٦	ERB2_MOUSE	P70424	mus musculu
18	723		-	-	ILPR_BRALA	002466	branchiosto
19	703	10.3	1300	-	IRR MOUSE	09wt14	mus musculu
50	697	10.2	1607	-	MIPR LYMST	025410	lymnaea sta
21	692	10.2	1297	-	IRR HUMAN	P14616	homo ganien
22	691	10.2	1383	-	INSR_RAT	P15127	rattus norv
23	686.5	10.1	1300	-	IRR_CAVPO	P14617	cavia porce
24		10.1	1382	٦	INSR HUMAN	P06213	homo gapien
25	682.5	10.0	1372	-	INSR_MOUSE	P15208	mus musculu
26	678	10.0	1477	-	HTK7_HYDAT	025197	hydra atten
27	641	9.4	1367	-	IG1R_HUMAN	P08069	homo sapien
28	623	9.5	1373	-	IG1R_MOUSE	060751	mus musculu
29	62		2146	-	INSR_DROME	P09208	drosophila
30	619.5	٠	7	7	IG1R_RAT	P24062	rattus norv
31	619	•	σ	-	INSR_AEDAE	093105	aedes aegyp
32	9	8	987	~	EPB4_HUMAN	P54760	
13	5.665	8.8	984	-	EPB1_RAT	P09759	rattus norv

P54762 homo sapien	Q91736 xenopus lae	091571 xenopus lae	007494 gallus gall	P54761 mus musculu	O00944 gallus gall	P07949 homo gapien	003145 mus musculu	P29317 homo Bapien	O91738 xenopus lae	P53356 hydra atten	P34152 mus musculu
EPB1 HUMAN	EPBB_XENLA	EPBA_XENLA	EPB1 CHICK	EPB4 MOUSE	FAK1 CHICK	RET HUMAN	EPAZ MOUSE	EPA2 HUMAN	FAK1 XENLA	HT16 HYDAT	FAK1_MOUSE
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984	902	985	984	987	1053	1114	776	916	1068	757	1052
8.7	8.7	9.8	9.5	8.5	8.5	8.5	8.5	8.4	8.4	8.3	8.3
593.5	592	583.5	581.5	580	578.5	578	575.5	569.5	269	565.5	265

ALIGNMENTS



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YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT 360
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                ; Score 6651; DB 1; Length 1255;
; Pred. No. 0;
10; Mismatches 20; Indels 0;
                                                                                                                                                                                                                                                                                                                   P -> A (IN REF. 2).
MW; 39E9DFDA04DCF962 CRC64;
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/FTId=VAR_004078
                                                                                                                                                                                                                                                                                                                                                                     97.8%;
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Matches 1225; Conservative
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration the Ewropean the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000194; EGFR L domain.

InterPro; IPR000194; EGFR L domain.

InterPro; IPR0001245; Furin-like.

InterPro; IPR001245; TVL pkinase.

InterPro; IP
     PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON INCOME.
RESIDUES (BY SIMILARITY).
POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POLYMORPHISM: TALELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.206; SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
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PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                             EMBL; M11767; AAA35808.1; --
EMBL; M11762; AAA35808.1; --
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M1206; AAA35808.1; --
EMBL; M1206; AAA35808.1; --
EMBL; M1206; AAA35978.1; --
FIR; A24571; A24571.
FIR; A24571; A24571.
MIN; 164870; --
MIM; 164870; --
MIM; ERBEZ.
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901 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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                                                                                                  LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bargmann C.I., Hung M.-C., Weinberg R.A.; Inthe neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbs-2 precursor (EC 2.7.1.112)
(p185erbs2) (NEU proto-oncogene) (C-erbs-2) (Epidermal growth factor ERBs2 OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
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MEDLINE=92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1257 AA.
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TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed=3945311;
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MEDLINE=91222560; PubMed=2025425;
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Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
"Three dimensional structure of the transmembrane region of the protoconcedents and oncogenic forms of the neu protein.";
EMBO J. 11:43-48(1992)

-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREMEGULIN.

- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

tyrosine phosphate.

-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE

RESIDUES (BY SIMILARITY). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch). PIR, A43562; TVRTMU.

REALLY A44562; TVRTMU.

REALLY PIRSP. P1362; TVRTMU.

REALLY PROMOTO PIECK.

INTERPRO; IPROMOTO PIECK L. domain.

RICEPRO; IPROMOTO PIECK L. domain.

RICEPRO; IPROMOTO PIECK L. MACHINE.

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REALLY PROMOT KINASE ERBB-2. RECEPTOR PROTEIN-TYROSINE EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL) PROTEIN KINASE.
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                               WMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPSSPMDSTFYRSLLEDDDMGDLV
                                                                                                                                                                                                             VRLVHRDLAARNVLVKS PINHVK I TDFGLARLLDI DETEYHADGGKVP I KMMALESI LRRR
                                                    VRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRR
                                                                                                                                             WMIDSECRPRFRELVSEFSRMARDPORFVVIONEDLGPASPLDSTFYRSLLEDDDMGDLV
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MEDINE-94193007; PubMed=7908275;

MEDINE-94193007; PubMed=7908275;

MEDINE-94193007; PubMed=7908275;

Makamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,

Yamazaki Y., Ishikawa T.,

"Cloning and activation of the Syrian hamster neu proto-oncogene.";

"Cloning and activation of the Syrian hamster neu proto-oncogene.";

Gene 140:251-2551194).

"FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

ATTHOGHY NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A

POTENTIAL LIGAND FOR THIS RECEPTOR.

ALPHA AND AMPHIREGULIN (BY SIMILARITY).

"CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
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SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNS-2002 (Rel. 41, Last annotation update)
15-UNS-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (PBSecbB2) (NEU proto-oncogene) (C-erbB-2).
ERBB2 OR NEU.
Mesocricetus auratus (Golden hamster).
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R HSSP; P11362; 1FGK.

R HCEPPC; IPR000194; Euk_pklnase.

R InterPro; IPR000145; Furin-like.

R InterPro; IPR000145; Tyr_pklnase.

R InterPro; IPR00145; Tyr_pklnase.

R InterPro; IPR00145; Tyr_pklnase.

R InterPro; IPR00145; Tyr_pklnase.

R InterPro; IPR00169; Euk_pklnase.

R Fdam; PF00157; Furin-like; 1.

R Fdam; PF00177; YLD; 2.

R Fdam; PF0130; Recept_domain; 2.

R ProDom; PD000001; Euk_pkinase; 1.

R PROMATT; SM00201; FU; FU; 3.

R PROSTTE; PS00107; PROTEIN KINASE TYP; 1.

R PROSTTE; PS0011; PROTEIN KINASE TYP; 1.

R PROSTTE; PS0011; PROTEIN KINASE DOM; 1.
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ities requires a license agreement (send an email to license@isb-sib.ch)
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9 85.9%; Score 5846.5; DB 1; Length 1254; 85.7%; Pred. No. 6.4e-307; ive 65; Mismatches 114; Indels 1; Conservative Best Local Similarity Matches 1075; Conserv Match Query

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IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020 360 540 120 120 180 240 240 300 300 420 420 480 480 540 900 9 9 9 720 720 780 780 840 840 900 900 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC **ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG** LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC **AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP ELEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEE1TGYLY1SAWPDSLP** IQEFAGCKKIFGSLAFLPESFDGNPSSGIAPLTPEQLQVFETLEEITGYLYISAWPDSLH PWDQLFRNPHQALLHTANR PEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC RKVKVLGSGAFGTVYKGIWI PDGENVKI PVA I KVLRENTSPKANKE I LDEAYVMAGVGSP YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM 181 181 361 541 1021 61 121 241 241 301 301 361 421 481 541 601 661 661 841 841 901 1021 1081 1081 121 421 481 601 721 721 781 781 901 961 961

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1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-84219729; PubMed=6128312;
WILTICH A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whitle N., Waterfield M.D., Seeburg P.H.;
"Human epidermal growth factor receptor cDNA sequence and aberrant
expression of the amplified gene in A431 epidermoid carcinoma cells.";
Nature 309:418-425(1984).
                                                 1201 GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                              EGFR HUMAN STANDARD; PRT; 1210 AA. P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732; O00688; Q9BES2; Q9PAC9; Q9GEX1; Q9H3C9; Q00688; Q9PES2; Q9PAC9; Q9CX1; Q9H3C9; Q1-UUL-1986 (Rel. 01, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-UNA-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor EGFR OR ENBB1.
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MEDLINE=21100872; PubMed=11161793;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A., Schell Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.! Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D., Maihle N.J.;
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative genomic sequence analysis and isolation of human and mouse alternative EGFR transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95382957; PubMed=7654368;
Ilekis J.V., Stark B.C., Sococia B.;
"Possible role of variant WA transcripts in the regulation of
epidermal growth factor receptor expression in human placenta.";
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"Expression of a truncated epidermal growth factor receptor-like
protein (TEGRN) in ovarian cancer.";
Gynecol. Oncol. 65:36-41(1997).
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Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
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MEDLINE=97078686; PubMed=8918811;
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Mroczkowski B., Mosig G., Cohen S.;
"ATP-stimulated interaction between epidermal growth factor receptor
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MEDLINE=85270438; PubMed=2991899;
Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.
"Characterization and sequence of the promoter region of the human epidermal growth factor receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
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                                                                                                                                                                                       SEQUENCE OF 713-924 FROM N.A. MEDLINE=84196372; PubMed=6326261; Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W., Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.; "Expression cloning of human EGF receptor complementary DNA: gene amplification and three related messenger RNA products in A431
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Biochem. Biophys. Res. Commun. 124:125-132(1984).
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MEDLINE=85046483; PubMed=6093780;
Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
O'Malley B.W.;
Maihle N.J., "Human and mouse alternative EGPR transcripts encoding only "Human and mouse alternative \rm EGPR
                                                                       extracellular domain of the receptor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variety of RNAs overproduced in A431 carcinoma cells."
Nature 309:806-810(1984).
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Kohda D.;
Submitted (SEP-1997) to the SWISS-PROT data bank
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J. Biol. Chem. 266:1746-1753(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 224:843-848(1984).
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Nature 309:270-273(1984).
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                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-98225196; PubMed=5556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
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FUNCTION: Receptor for EGF, but also for other members of the EGF femily, as TGF-appha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor. GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.

FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                   MEDLINE=96398132; PubMed=8962717;
Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
"Analysis of the glycosylation patterns of the extracellular domain
the epidermal growth factor receptor expressed in Chinese hamster
ovary fibroblasts.";
                                                                                                                                                                                                                                                                   atypical
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ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/
LTUNCATED isoform/TEGFR, 3/p110 and 4; are produced by
alternative splicing.
TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                                       Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D., "Characterization of the N-oligosaccharides attached to the aty Asn-X-Cys sequence of recombinant human epidermal growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
  ASN-175; ASN-413; ASN-444
                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Receptors for epidermal growth factor and other polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
SITES ASN-128;
                                                                                                                                                                                                 ASN-603.
MEDLINE=20198209; PubMed=10731668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW.
MEDLINE=87297456; PubMed=3039909;
                                                                                                                                         Growth Factors 13:121-132(1996)
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EMBL; U49722; AA650802.1; -.
EMBL; U48723; AAC50804.1; -.
EMBL; U48723; AAC50804.1; -.
EMBL; U48724; AAC50796.1; -.
EMBL; U48725; AAC50797.1; -.
                                                                                                                                                                                                                                                                                                                   Biochem. 127:65-72(2000).
CARBOHYDRATE-LINKAGE
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                                             VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR
                                                           |---ANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNH
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Indels 108;

Length 1210;

Query Match
45.8%; Score 3114; DB 1;
Best Local Similarity 49.6%; Pred. No. 4.4e-160;
Matches 628; Conservative 173; Mismatches 357;

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 Eisinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
STRAIN=84170986; Pubmed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
"The mouse waved-2 phenotype results from a point mutation in the EGF receptor tyrosine kinase.";
                                       1200 QGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP-----PERGAPPSTFKGTPTA
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINE-BALB(C, and CD-1; TISSUE=Liver, and Decidua;
STRAINE-BALB(C, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE-93126380; Pubmed-7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91232866; PubMed=2030916;
Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
"Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                   Eukaryota, Metazia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                            STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=91026370; PubMed=1408137;
MYOIVI A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor (bek/KGFR) gene.";
                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
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STRAIN=BALB/c; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                Oncogene 7:1957-1962(1992).
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                                                                                                   1193 ENAEYL 1198
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseasisb.shb.ch).
tyrosine phosphate.

SUBCELLUIAL LOCATION: Type I membrane protein.

MUSCELLANBOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell proliferation.

Synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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R InterPro; IPR000494; Egfr. L domain.

InterPro; IPR000194; Euk pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R Pfam; PF000069; Pkinase; 1.

R Pfam; PF000069; Pkinase; 1.

R Probom; Pp000069; Pkinase; 1.

R Probom; Pp0000019; Euk pkinase; 1.

R PR021TE; PS00109; PROTEIN KINASE ATP; 1.

R PR051TE; PS00109; PROTEIN KINASE TYR; 1.

R PR051TE; PS00119; PROTEIN KINASE DOM; 1.

R PR051TE; PS00119; PR0TEIN KINASE DOM; 1.
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EMBL, L06864; AAA53029.1; -
EMBL, Z12608; CAA78249.1; -
HSSP; P11362; IFGK.
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AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPE 1138
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    VSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRL
                                                          VHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTH
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MEDLINE=93189574; PubMed=8383326;
Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G.W., Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HER4/p180erbB4, a fourth member of the epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                                                                                                                     QSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMI
                                                                                                                                                                                                        DSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific tissue distribution and differential processing in response to phorbol ester.";
J. Biol. Chem. 272:26761-26768 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDILIRE=97476287; Pubmed=9334263;
Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.1
(P180erbB4) (Tyrosine kinase-type cell surface receptor HER4)
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1191 TAENAEYLRVAPP 1203
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(AUTO-, MAJOR SITE)
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-:- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND
NATAK. ITHERACTION WITH THESE PACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF, TGF-A, AND AMPHIRECULIN.
-:- CATALYTIC ACTIVITY: ATP + a Protein tyrosine = ADP + protein
-:- CATALYTIC ACTIVITY: TFP + a Protein tyrosine = ADP + protein
-:- SUBUNIT: HOWDDIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
-:- SUBCELLULAR LOCATION: Type I membrane protein The OTHER ERBB RECEPTORS (POTENTIAL).
-:- ALTERNATIVE PRODUCTS: Z ISOFORMS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESED IN THE HEART.
-:- TISSUE SPECIFICITY: EXPRESSED AT HIGHERS IN SEXPRESSED IN THE HEART;
KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHROID, CERBEBLLUM, LUNG, SALIVARY GLAND, AND PANCREAS.
-:- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of There are no restrictions on its wase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
CYS-RICH.
CYS-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
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R InterPro; IPR000199; Euk pkīnase.
R InterPro; IPR000119; Euk pkīnase.
R InterPro; IPR0001214; Fvrīn-like.
R InterPro; IPR0004019; Yup—motif.
R InterPro; IPR0004019; Yup—motif.
R InterPro; IPR0004019; Yup—motif.
R Ffam; PF001050; Recep L_domain; 2.
R Pfam; PF001757; Yup; 2.
R Prodom; PF0010001; Euk pkinase; 1.
R Prodom; PF0010001; Euk pkinase; 1.
R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
R RROSITE; PS00110; PROTEIN KINASE DOM; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R PROSITE; PS00101; PROTEIN KINASE DOM; 1.
R Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERBB4.
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### STMILARITY. ### No-Linked (GLCNAC) (POTENTIAL). ### STMILARITY. ### No-Linked (GLCNAC) (POTENTIAL). ### STMILARITY. ### STMILAR	tch al Similarity 45.2%; Pred. No. 1.4e-151; 609; Conservative 181; Mismatches 383; Indels 173; Gaps 28;	9 WGLLIALIPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYGGCQVVQGNLELTY 64	65 LPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN 124 :	125 NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI 184 	185 DTNRSRACHPCSPWCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG 243	244 CTGPKHSDCLACLHFNHSGICELHCPALVIYNTDTFESMPNPEGRYTFGASCVTACPYNY 303 1:	304 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE 363 :	364 FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS 423 1	424 VFONLOVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD 483	484 QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE 543	544 CRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPQ 602
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                                                                                     GLQGANSFIFKYADPDRE--CHPCHPNCTQGCNGPTSHDCIYYPWTGHSTLPQHAR-TPL
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SEQUENCE OF 1031-1198 FROW N.A.

SEQUENCE OF 1031-1198 FROW N.A.

STRAIN=Sprague-Dawley; TISSUE=Spinal cord;

MEDINE=97184212; PubMed=9030624;

RA MEDINE=97184212; PubMed=9030624;

RA Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RA Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RT ExbB3, is induced during Wallerian degeneration.";

J. Neurosci. 17:1642-1659(1997).

-1- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-C. NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NATA: INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

CC. -1- CATALYTIC ACTIVATES BY GFF-A, AND AMPHIREGULIN (BY SIMILARITY).

CC. -1- CATALYTIC ACTIVITY: ATP + a procein tyrosine = ADP + protein

CC. -1- SUBGELLULAR LOCATION: Type I membrane protein.

CC. -1- SUBGELLULAR LOCATION: Type I membrane protein.

CC. -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING

CC. -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING

CC. -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING

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CC. -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE BATTERNS

CC. -1- TISSUE SPECIFICITY: PREFERENTIALLY AND HIGHLY REGIONALIZED PATTERNS

CC. -1- TISSUE SPECIFICITY: PREFERENTIALLY WHERE IT IS MAINLY FOUND IN THE PREFERENTIAL AND HIGHLY BRAIN, WHERE IT IS MAINLY FOUND IN THE PURLY HIGHLY WARTHY AND THE PREFERENTIAL AND THE PREFERENTIAL AND THE PREFERENTE AND THE PREFERENTIAL AND THE PREFERENTIAL AND THE PROFESSED IN THE PREFERENTIAL AND THE PROFESSED IN THE PROFE

"An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).

Marchionni M.A., Kelly R.A.; "Neuregulins promote survival and growth of cardiac myocytes. Persistence of Erbb2 and ErbB4 expression in neonatal and adult ventricular myocytes.";

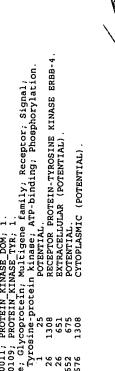
Biol. Chem. 273:10261-10269(1998)

TISSUE-Sciatic nerve; MEDLINE-91222560; PubMed-2025425;

C., Lemke G.;

SEQUENCE OF 848-901 FROM N.A.

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R InterPro; IPR000199; EUK_DEInase.
R InterPro; IPR000119; EUK_DEInase.
R InterPro; IPR001214; FUXin-like.
R InterPro; IPR001214; FUXin-like.
R InterPro; IPR001214; FUXIn-like;
R InterPro; IPR00129; YLP_monif.
R Fam; PR00137; FUXIn-like; 1.
R Fam; PR00137; FUXIN-Like; 1.
R Fam; PR00139; YLP_monif.
R Fam; PR00109; TYRKINASE.
R PRINTS; PR00109; TYRKINASE.
R PRODM; PR00109; TYRKINASE.
R PROSITE; PR00109; TYRKINASE.
R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS0010; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS0010; PROTEIN_KINASE_TYR; 1.
R Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
FIGNAL 1.25 POPERNIA MINAME TATE.
FULL TATES RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL). PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY. CYTOPLASMIC (POTENTIAL). EMBL; AF041838; AAD08899.1; -. EMBL; U52531; AAC53051.1; -. HSSP; P11362; 1FGK. DOMAIN TRANSMEM DOMAIN CHAIN



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;

Rattus norvegicus (Rat).

TISSUE=Heart; MEDLINE=98221155; PubMed=9553078; Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X.,

SEQUENCE FROM N.A.

062956; Q922N7; 15-DEC-1998 (Rel. 37, Created) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112) ERBB4 OR TYRO-2.

1308 AA

ERB4 RAT

RESULT 7 ERB4 RAT

157 IOTELERACIEKT FOSILAFIZES FOODPASHTRELOPEGIOVERILES ITOLINISANE 416 249 DESISTION THE THE PRINCE AND AND ASSET TO THE PRINCE AND ASSET AND ASSET AND ASSET TO THE PRINCE AND ASSET AND ASSET AND ASSET AND ASSET AND ASSET ASSET AND ASSET ASSET AND ASSET AND ASSET ASSET AND ASSET ASSET ASSET ASSET ASSET ASS	RESULT 8 XMRK_XIPMA ID XMRK_XIPMA STANDARD; PRT; 1167 AA. AC P13388;
DOMAIN 186 334 CYS-RICH.	ANSKF : SAQTV

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DR PIR; S06142.

DR PIR; S06142.

DR INTERPO; IPR000494; EGFR L domain.

DR INTERPO; IPR00019; Euk pkinase.

INTERPO; IPR002199; Euk pkinase.

DR INTERPO; IPR001245; Tyr_pkinase.

DR INTERPO; IPR001245; Tyr_pkinase.

DR Fam; PF001069; pkinase; 1.

DR Pfam; PF00109; TwkINASE.

DR PRONTS; RM00261; Fuk pkinase; 1.

DR PRAMT; SM00220; STKC; 1.

SWART; SM00220; STKC; 1.

DR SWART; SM00220; STKC; 1.

SWART; SM00220; STKC; 1.

DR SWART; SM00220; STKC; 1.

SWART; SM00220; STKC; 1.

SWART; SM00220; STKC; 1.

CW SWART; SM0019; TWKC; 1.

DR SWART; SM0019; TWKC; 1.

DR SWART; SM0019; TWKC; 1.

CW TYTOSINE-PROFIEN KINASE DOM; 1.

CW TYROSINE-PROFIEN KINASE DOM; 1.

CW TYROSINE-PROFIEN KINASE DOM; 1.

TYROSINE-PROFIEN KINASE DOM; 1.

TYROSINE-PROFIEN KINASE; ATP-binding; Phosphorylation; Proto-oncogene.

THE STANDARD STANDARD AND STANDARD AND STANDARD 
                                                                                                                                                                                                                                                                                                                                                                                                                                            Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112)
                                                                                           hiphophorus maculatus (Southern platyfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Cyprinodontiformes, Poeciliidae, Xiphophorus.
                                                                                                                                                                                                                                 MELANOMA RECEPTOR PROTEIN-TYROSINE

tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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EXTRACELLULAR (POTENTIAL)
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DISULFID 237 245 BY SIMILARITY. DISULFID 241 253 BY SIMILARITY. DISULFID 256 265 BY SIMILARITY. DISULFID 300 311 BY SIMILARITY. DISULFID 313 BY SIMILARITY. DISULFID 504 513 BY SIMILARITY. DISULFID 508 S21 BY SIMILARITY. DISULFID 524 533 BY SIMILARITY. DISULFID 556 S69 BY SIMILARITY. DISULFID 556 S77 BY SIMILARITY. DISULFID 556 S77 BY SIMILARITY. DISULFID 556 S77 BY SIMILARITY. DISULFID 560 S77 BY SIMILARITY. DISULFID 560 S77 BY SIMILARITY. DISULFID 618 BY SIMILARITY. DISULFID 618 BY SIMILARITY. DISULFID 619 BY SIMILARITY. DISULFID 614 N-LINKED (GLCNAC) (POTENTIAL). <th>Query Match 39.1%; Score 2657.5; DB 1; Length 1167; Best Local Similarity 45.0%; Pred. No. 1.4e-135; DB 1; Length 1167; Gaps 29; Matches 570; Conservative 167; Mismatches 392; Indels 139; Gaps 29; Handels 139; Length 1167; Indels 139; Gaps 29; Handels 139; Length 139; Caps 29; Handels 139; Length 14, Length 14, Handels 139; Length 14, Length 14, Handels 139; Length 139; Length 139; Handels 14, Length 14, Length 14, Handels 14, Length 14, Length 14,</th> <th>20 GD 23 YQ 80 AL 80 TM 39 QC 140 HC</th> <th>99 CPNYLSTDVGSCTLVCPLHNOEVTAEDGTQRCEKCSKPCARVCYGLGMOYIKANSKFIG 35 0</th> <th>530 GGKCVASCNLLQGEFKEAQVDGKCVQCHQECLVQTDSLTCYGFGPANCSKSAHFQDGPQC 589 597 VARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 656</th>	Query Match 39.1%; Score 2657.5; DB 1; Length 1167; Best Local Similarity 45.0%; Pred. No. 1.4e-135; DB 1; Length 1167; Gaps 29; Matches 570; Conservative 167; Mismatches 392; Indels 139; Gaps 29; Handels 139; Length 1167; Indels 139; Gaps 29; Handels 139; Length 139; Caps 29; Handels 139; Length 14, Length 14, Handels 139; Length 14, Length 14, Handels 139; Length 139; Length 139; Handels 14, Length 14, Length 14, Handels 14, Length 14, Length 14,	20 GD 23 YQ 80 AL 80 TM 39 QC 140 HC	99 CPNYLSTDVGSCTLVCPLHNOEVTAEDGTQRCEKCSKPCARVCYGLGMOYIKANSKFIG 35 0	530 GGKCVASCNLLQGEFKEAQVDGKCVQCHQECLVQTDSLTCYGFGPANCSKSAHFQDGPQC 589 597 VARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS 656
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owman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
                                                                                                                     SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M29366; AAA35790.1; -. EMBL; M34309; AAA35979.1; -. EMBL; S61953; AAB26935.1; -.
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SIGNAL 1
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                                                                                                                                          TISSUE-Placenta;
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MIM; 190151;
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                                                                                  ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAG 776
                                                                                                                                                                                                                                                                                                      EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR 896
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                                                                                                                                                             AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(c-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90083234; PubMed=2687875; Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.; Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.; Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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MEDLINE=90311312; PubMed=2164210;
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P21860;
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InterPro; IPR000419; Euk_pkinase.
InterPro; IPR00174; Purin-like.
InterPro; IPR001245; Tyr_pkinase.
INTERPRO; IPR00124; Interpro; Interpro; IPR Propon, PD000001; Euk_pkinase; 1.
INTERPRO; SM00219; TyrKc; 1.
INTERPRO; IPRO; IPRO; INTERPRO; INTERPRO; IPRO; IPRO; INTERPRO; INTERPRO; IPRO; IPRO; INTERPRO; IPRO; INTERPRO; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECRETED (SHORT FORM).

ALTERNATIVE PROBUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
DOWAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LICAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PAS SUBUNIT OF PROMOTES ITS ASSOCIATION WITH THE MAS SUBUNIT OF PROBENTRINGS.

PHOSPHORES OVEREXPRESSED IN A SUBSET OF HUMAN MAWMARY TUMORS.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELULAR (POTENTIAL).
Odaro G.J., Shoyab M.;
Molecular cloning and expression of an additional epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate. SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                factor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
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MIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPA---SPLDSTFYRSLL 1009
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                                                                                                                                                                                  654 IVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQM
           DOLPRNPHOALLHTA-NRPEDECVGEGLACHOLCARGHCWGPGPTOCVNCSQFLRGQECV
                             EECRVLOGLPREYVNARHCLPCHPECOPONGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                     531 THCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
                                                                                                                          QYIKANSKFIG----ITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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ID ERB3 RAT

AC Q62799; Q62955;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-UNN-2002 (Rel. 41, Last sequen
DT 15-JUN-2002 (Rel. 41, Last sequen
DT 15-JUN-2002 (Rel. 41, Last sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U29319; AAC33050.1; ...

REMBL; U29319; AAC33050.1; ...

REMPL; U32510; AAC33050.1; ...

RESP, U31362; LFGK.

InterPro; IPR000494; EGFR L domain.

RITHERPO; IPR000179; EUK_pkinase.

RITHERPO; IPR001245; TYL_pkinase.

RITHERPO; IPR001245; TYL_pkinase.

REAM; PF001030; RECEP_L domain; 2.

REAM; PR00109; TYRKINASE.

REAM; SM00201; FU; S.

RAMAT; SM00201; FU; S.

RAMAT; SM00201; FU; S.

RAMAT; SM0019; TYKC: 1.

ROSITE; PS00109; PROTEIN KINASE_ATP; FALSE_NEG.

RROSITE; PS00109; PROTEIN KINASE_ATP; FALSE_NEG.

RROSITE; PS00109; PROTEIN KINASE_ATP; TALSE_NEG.

TRANSFERE PS00109; PROTEIN KINASE_ATP; TALSE_NEG.

RROSITE; PS0011; PROTEIN KINASE_ATP; TALSE_NEG.

TRANSFERE PS00109; PROTEIN KINASE_ATP; FALSE_NEG.

TRANSFERE PS00109; PROTEIN KINASE_DOM; 1.

RAMATS TANSFERE TALSE_NEG.

TRANSFERE PS00109; PROTEIN KINASE_DOM; 1.

TRANSFERE PS00109; PROTEIN KINASE_DOM; 1.

TRANSFERE PS00109; PROTEIN KINASE_DOM; 1.

TRANSFERE TALSE_NEG.

TRANSFERE PS00109; PROTEIN KINASE_DOM; 1.

TRANSFERE TALSE_NEG.

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TRANSFERE TALSE_NEG.

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TRANSFERE TALSE_NEG.
                                                                                                                                                                                                                                                                                               (POTENTIAL).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- DOMAIN: THE CYTOFLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3. KINASE.

-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                            SEQUENCE OF 922-1097 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
STRAIN=Sprague-Dawley; TISSUE=Sciatic nerve;
MEDINNES-97184212: PubMed=9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Mallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-i- CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                           J.G.
                                                                                                                                                                                                                                                                    tyrosine phosphate.
STRAIN=Sprague-Dawley, TISSUE-Liver;
BEDLINE-S6096535; Pubhed-ed-852120,
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland
"Cloning of the rat ErbB3 cDNA and characterization of the
                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
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584 HCVNSCPHGI-----LGAKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEVLM 637
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C P04412; OG1601; O9W2G0; P81868;
T 13-AUG-1987 (RR1. 05. Created)
T 15-DEC-1998 (RR1. 37. Last sequence update)
T 16-OCT-2001 (Rel. 40. Last annotation update)
T 16-OCT-2001 (Rel. 40. Last annotation update)
E Bpidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)
E Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB).
N Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB).
S C Gurkeyyota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
C Musecomorpha; Ephydroidea; Drosophilidae; Drosophila.
N NCBI_TaxID=722;
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MEDLINE=94350209; Pubmed=8070664;
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A CLIfford R. Schubbach T. Schubbach T. Strucker G. Schubbach T. Stubiltod R. Schubbach T. Stubiltod R. Schubbach T. Stubiltod R. Schubbach T. Schub
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                                                                                                                                                                                                                                                                             EGF receptor.";

Cell 89:13-16 (1997).

Lebuction: Bloom Ligands: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.

CRITICAL FOR THE PROLIFERATION OF INMAINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTEANNES OF AMNIOSEROSA AND VENTRAL NEUROBETODERMAL CELLS, GERM BAND RETRACTION, CELL FATES SPECIFICATION IN THE CENTRAL NEUVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE II; ARE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                     SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                    [9]
REVIEW.
MEDLINE=97248481; PubMed=9094709;
Pertimon N., Perking L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
                                                                       ANALYSIS.
MEDLINE-92038942; PubMed=1936959;
Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K03054; AA51462.1; ...
K03416; AA51460.1; ...
K03416; AA51965.1; ...
K03418; AA51961.1; ...
AF109077; AAD26134.1; ...
AF109078; AAD26132.1; JOINED.
AF109078; AAD26133.1; ...
AF109078; AAD26133.1; ...
AF109078; AAD26130.1; ...
AF109081; AAD26130.1; ...
AF109083; AAD26130.1; ...
AF109083; AAD26131.1; ...
AF109080; AAD26131.1; ...
AF109080; AAD26131.1; ...
AF109080; AAD26131.1; ...
AF109080; AAD26131.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF052754; AAC08536.1; -.
EMBL, AF052753; AAC08536.1; JOINED.
EMBL, AF052754; AAC08535.1; JOINED.
EMBL, AF052752; AAC08535.1; JOINED.
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growth factor receptor.";
                 Nature 314:178-180 (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | | : | | : | | : | PQDXMDKGGE-----CVPCNGPCPKTC------PGVTVLHAGNIDSFRNCTV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 IFGSLAFLPESFDG--DPASNTA-----PLQPEQLQVFETLEEITGYLYISAWPDSLPD 421
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                      Phosphorylation; Transferase;
                                                                                                                                                                                                                                                                   Transmembrane; Glycoproteīn; Recēptor; Phosphorylation; Transferase
Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing;
Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 28.6%; Score 1947; DB 1; Length 1426; Best Local Similarity 32.7%; Pred. No. 2.8e-97; Matches 467; Conservative 182; Mismatches 433; Indels 346;
                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                    InterPro; IPR000494; EGFR L domain.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000119; ENK pkinase.
InterPro; IPR00174; Furin-like.
InterPro; IPR001245; TYr pkinase.
Pfam; PF00105; pkinase; I.
Pfam; PF00105; Pkurin-like; I.
Pfam; PF00105; Pkurin-like; I.
Pfam; PF00109; TYRKIMASE.
PRODm; PR00109; TYRKIMASE.
PRODm; PR00109; TYRKIMASE.
PROSTITE; PS00107; PROTEIN KINASE ATP; I.
PROSTITE; PS00109; PROTEIN KINASE TYR; I.
PROSTITE; PS00109; PROTEIN KINASE DOM; I.
                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                            FlyBase; FBgn0003731; Egfr.
EMBL; X78919; CAA55522.1;
PIR; A00640; GQFFE.
HSSP; P11362; 1FGK.
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889
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TRANSMEM
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seq4-579-593-12.rsp

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: : : : IADCGYISNAYKPDNRTCKI	PQY I KANSK	PKN-KYNDRGVCRECHATCDGC										VYKGVWVPEGENVKIPVAIKEL	VOLVTOLMPYGCLLDHVRENRG	MMLITQLMPLGCLLDYVRNNRD	KSPNHVKITDFGLARLLDIDETI	OTPSLVKITDFGLAKLLSSDSN	ELMTFGAKPYDGIPAREIPDLLI	ELLTFGQRPHENIPAKDIPDLI	SEFSRMARDPORFVVIONEDLG	TVFABFARDPGRYLAIPGDKFTF	GFFCPDPAPGAGGMVHHRHRSSS	: DYLQPKAAPGPSHRTDC	SDVFDGDLGMGAAKGLQSLE	DDERDSSAREVGVGNLR	VNQPDVRPQPPSPREGPLPAARP	NNNMNNPNQNNMAAVGVAAGYM-	TPQGGAAPQPH	AQTLGVGESPIPTQTIGIPVMGG
603	601	655	617	714	633	774	643	834	919	892	734	952	794	1012	854	1072	914	1132	974	1192	1029	1245	1083	1284	1140	1322	1198	1361
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REMEL; M10066; AAA48763.1; ALT_INIT.
R PIR; A00643; TVCHLV.
R PIR; B00643; TVCHLV.
R HSSP; P11362; IFGK.
R INTERPO: IPR000719; Euk pkinase.
R INTERPO: IPR00059; PXINASE.
R PRIM; PR00109; TYRINASE.
R PRIMTS; PR00109; TYRINASE.
R PRODOM; PR00109; TYRINASE.
R PROSTITE; PS00109; PROTEIN KINASE ATP; 1.
R PROSTITE; PS00109; PROTEIN KINASE TYR; 1.
R PROSTITE; PS0011; PROTEIN KINASE DOM; 1.
TRANSFERRESE; TYSCBING-PROCEIN KINASE DOM; 1.
TRANSFERRESE; TYSCBING-PROCEIN KINASE DOM; 1.
TRANSFERRESE; TYSCBING-PROCEIN KINASE DOM; 1.

70891 MW; E705E33A0BE01FCC CRC64;

ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY. PROTEIN KINASE

146 165 257

BINDING ACT SITE SEQUENCE

Phosphorylation.

Glycoprotein; DOMAIN

BIND

LYTOSINE phosphare.

-!- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

Cell 41:719-726(1985)

RNA

Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Raines M.A., Kung H.-J.; "c-erbB activation in ALV-induced erythroblastosis: novel processing and promoter insertion result in expression of amino-truncated EGF receptor.";

MEDLINE=8522822; PubMed=2988784;

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17;
                                                             646
                                                                                                                   705
                                                                                                                             59 NGSKIPSIAAGWUGGLLCLWVVGLGIGLYLRRR-HIVRKRILRRLLOBRELVEPLIPSGE 117
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                                                                                                                                                                                  EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW 825
                                                                                                                                                                                                                                        CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP 885
                                                                                        58
                                                                                                                                                                                                                                                                                             886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGBRLPQPP 945
                                                                               3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                      587 CAHYKDPPFCVARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                            647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                  706 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                     Gaps
               51.8%; Pred. No. 1.8e-85;
ive 79; Mismatches 139; Indels 123;
  25.3%; Score 1719.5; DB 1; Length 634;
                            366; Conservative
               Similarity
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21-JUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).

634 AA

PRT;

STANDARD;

ERBB ALV P00534; Avian leukosis virus. Viruses; Retroid viruses; Retroviridae; Alpharetrovirus. NCBI_TaxID=11864;

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NP BIND
BINDING
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CONFLICT
CONFLICT
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                                                                                                                                                                    1064
                                                                                                                                                                                                                                                                .065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
                                                                                                                                                                                                                                                                                                                                                         1120 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1178 NGVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY 1222
                                                                                                                    417
                                                                                                                                                                                                                   449
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                                                                                                                                                                                                                                                                                                                                                                                                           526
Science 224:1456-1459(1984).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS IN CHICKENS.
                                                                                                                                                                                                                                                                                                                                                                                       496 FLEESIDDGFL-----TAMPEYVNQ-LMPKKPS-----TAMVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.;
src
                                                                        ICTIDVYMIMVKCMMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF
                                                                                                   358 ICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMHLPSPTDSKF
                                                                                                                                                                    1005 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                                                                                                                                                                                                                                                                                              NOIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFESSPY
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MEDLINE=84223957; PubMed=6328658;
Debuire B., Henry C., Benaissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals new type of oncogene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84026539; PubMed-6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima
"The erbB gene of avian erythroblastosis virus is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C.
NCBI_TaxID=79685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGBRLPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   946 ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 -----SRTPLLSSLSATSNNSATNCID------RNGQGHPVREDSFVQRYSSDPTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ICTIDVYMIMVKCWMIDADSRPKPRELIAEFSKWARDPPRYLVIQGDERWHLPSPTDSKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.8%; Score 1688; DB 1; Length 604;
51.7%; Pred. No. 8.6e-84;
ive 76; Mismatches 131; Indels 126;
                                                                                                                                                                                 SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

R -> W (IN REF. 2).

S -> F (IN REF. 2).

I -> V (IN REF. 2).

Y, 76BGCDD06745D609 CRC64;
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EMBL; KO2006; AAA42394.1; ALT_INIT.
BERL; KO1216; AAA42400.1; -.
PIR; AO0644; TVVUH.
HSSP; P11362; 1FGK.
                                                                                      InterPro; IPR000719; Buk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I
ProDom; PD000001; Buk pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                 165 165 AT 257 BY 257 257 BY 29 R 140 140 S 146 146 S 1 604 AA; 67633 MW;
                                                                                                                                                                                                                                                                                                     Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 51.7<sup>1</sup>
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                     Glycoprotein;
DOMAIN 13
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seq4-579-593-12.rsp

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1179 GVVKDVFAFGGAVENPEYL 1197
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MEDLINE=88261272; PubMed=3260329;
                                                                                                                                                                                                                                                                                                                                         539
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-----SHSTAVDNPEYL
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                              CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                      P13387;
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CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                SEQUENCE FROM N.A. McDAmed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587 CAHYKDPPFCVARCPQYIKANSKFIGITELPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EILDEAYVMAGVGSPYVSRLLGICLTSTVOLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90; Gaps
                                                                                                                                                viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                      Mol. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                    01-JUL-1989 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene; Glycoprotein; Phosphorylation.
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H -> D (IN THERMOLABILE V-ERBB).
; 5B53297AA068B65D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                            tyrosine phosphate.
-- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123;
                                                             Ź
    ----INLDNPDY 594
                                                                                                                                        virus (strain ts167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Mismatches
                                                            540
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, M13179, AAA42401.1; -. PTR; A25231; TVFVEB.
HSSP, P11362; 1FCK.
InterPro; 1PR000719; Euk pkinase.
InterPro; 1PR001245; Tyr pkinase.
ProDom; PD000001; Euk pkinase; 1.
                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seg
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60412 MW;
 575 SSPYWIQSGNHQ-----
                                                         STANDARD;
                                                                                                                                     erythroblastosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00219; TyrKc;
                                                                                                                                                             NCBI_TaxID=103898;
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                                                                                                                                                 Viruses; Retroid
                                                        ERBB AVIEU
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Matches 337;
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VARIANT
SEQUENCE
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                                                                 P11273;
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                                         EMBL; M20386; AAA48760.1; -.

R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R Pfam; PF00757; Furin-like; 1.
R Pfam; PF00103; Recept L domain; 2.
SMART; SM00261; FU; 4.— Omain; 2.
R PROSITE; PS00107; PROTEIN KINASE TYR; PARTIAL.
R PROSITE; PS00107; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS00109; PROTEIN KINASE DOM; PARTIAL.
R PROSITE; PS00109; PROTEIN KINASE DOM; PARTIAL.
R Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
Tyrosine-protein kinase; ATP-binding; Phosphorylation.
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email to license@isb-sib.ch)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O18735 canis famil	O90x70 rattus norv	O9ep98 mus musculu	O9yh40 xiphophorus	O9w6f6 gallus gall	P79754 fugu rubrio	O9bih9 anopheles o	Oguk79 homo gapien	OBr2x1 mus musculu	086712 avian rous-	Q86714 avian rous-	OBwyv0 homo sapien	064895 avian ervth	085468 avian ervth	09wvf5 mus musculu	O9erv6 mus musculu
SUMMARIES	ID	018735	090X70	Q9EP98	Q9YH40	Q9W6F6	P79754	69ВІН9	Q9UK79	QBR2X1	086712	086714	Q8WYV0	064895	085468	Q9WVF5	O9ERV6
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1274	1182.5	1169	1108	1001.5	928.5	906	806.5	800	178	754.5	734	731.5	723	721	695	685.5	672.5	664.5	099	658	641.5	638	628	620.5	9	595	593	587.5
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ALIGNMENTS

	735 PRELIMINARY; PRT; 1259 AA. 735;	01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence undate)	(TrEMBLrel. 21, Last	B-2.	canis ramiliaris (Dog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	ia; Carnivora; Fissipedia; Canidae;	NCBI_TaxID=9615; [1]	SEQUENCE FROM N.A.	Yokota H.;	"cDNA cloning of erbB-2 from canine mammary gland.";	EMBL/GenBank/DDBJ datab	EMBL; AB008451; BAA23127.1;	362; 1FGK.	٠.	IPR000494;	IPR000719;	IPR002174;	IPR001245;	ero; IPRUC	m; Fround); Furin-like; 1. m. DROOMS: Skinses: 1	PF01030;	PF02757; YLP; 2	; PD0000	0,	RT; SM00219; TyrKc; 1.	SITE; PS00018; EF_HAND; UNKNOWN_1.	SITE; PS00107; PROTEIN_KINASE_ATP; 1.	PROSITE, PS50011; PROTEIN KINASE DOM; 1.	SITE; PS00109; PROTEIN KINASE TYR; 1.	-binding; Transferase; Tyrosine-protein kinase. Hence 1960 aa. 1990o ww. 1990ok	1259 AA;
RESULT 1	018735														InterPro;	InterPro;				Dfam. D					SMART;	PROSITE	PROSITE	PROSITE	PROSITE	ATP-bind	OBCODIAL.
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"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990).
 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                            NOPDVRPOPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGGAVENPE
                                                                                            LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; EUK_pKinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00110; PROTEIN KINASE TYR; 1.
ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE 1209 AA; 134891 MM; 96FEETF6CC1B7773 CRC64;
                                                                                                                                                                                                                                                                                                                                                              STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; Pubmed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FISHER; TISSUE=LIVER; Guttridge K., Dawson T.L., Earp H.S.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
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Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
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InterPro; IPP000719; Buk_pkinase.
InterPro; IPR001214; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP00757; Furin-like; 1.
Pfam; PP01030; Recep_L_domain; 2.
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STRAIN=FISHER; TISSUE=LIVER;
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HSSP; P11362; 1FGK.
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                                                                                         ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                     DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                             MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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Query Match 90.1%; Score 6129; DB Best Local Similarity 90.0%; Pred. No. 0; Matches 1134; Conservative 42; Mismatches
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1134 SPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN 1193
                                                                                                                                PEYLNTAQ-----PTCLSSGFDSSALWIQKGSHOMSLDNPDYQQDFFPKEAKPNGI 1185
                                                                                               PEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPST
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                                                      - PVPEYINO-SVPKRPAGSVQNPVYHNQPLHP-----APGRDLHYQN--PHSNAVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J. Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
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                                                                                                                                                                                                                                                                                                                   01-MAR.2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP: P11362; 1FGK.
MGD; MGI:95294; EGfr.
InterPro; P11362; IFGK.
MGD; MGI:95294; EGfr.
InterPro; IPR000345; CytC, heme_bind.
InterPro; IPR000194; EGFr_L domain.
InterPro; IPR0002104; Furin-like.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001045; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00100; Recep_L domain; 2.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00201; FU; 5.
SMART; SM00201; FVKC; 1.
PROSITE; PS00109; TYRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
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FKG-PTAENAEYLRVAPP 1202
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LAALCAAG-----GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
                                                                                                                                                                                                                                                             CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
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    DADSRPKFRELILEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMEDVVDA 1015
                                                                                                                ATSN----NSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAFL-----PVPE
                                                                                                                                                              TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPSTFKGTP
                               EEYLVPQQGFFCPDPAPGAGGMVHHRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                         ----SRTPLLSSLS
                                                                                      1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPE
                                                                                                                                                                                                                              TAQ------PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGIFKG-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Medazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C.; Wellbrock C., Gomez A., Duschl J.,
Altschmied J., Schartl M.;
Activation of the Xmrk proto-oncogene of Xiphophorus by
overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00757; Furin-like; 1.

Pfam; PF00069; pkinase; 1.

Pfam; PF001069; pkinase; 1.

R Pfam; PF00109; Recep_L domain; 2.

R PROBOM; PF00109; TYRKINASE.

R SMART; SM00219; TYRK; 1.

R SMART; SM00219; TYRK; 1.

R PROSITE; PS00199; CYTOCHROME C; UNKNOWN 1.

R PROSITE; PS00110; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE ATP; 1.

R PROSITE; PS00119; PROTEIN KINASE TYR; 1.

R PROSITE; PS00119; PROTEIN KINASE TYR; 1.

R PROSITE; PS00119; PROTEIN KINASE TYR; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                               PRT; 1165 AA
                                                           ---NSPST-
                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor tyrosine kinase proto-oncogene.
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR00019; Buk pkinase.
InterPro; IPR001194; Furin-like.
InterPro; IPR0011899; Gram pos anchor.
InterPro; IPR001245; Tyr pkinase.
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                                                                                                                                                                                                                                                          1242 TAENPEYLGLDVP 1254
                                                                                                                                                                                                                                                                                       TAENAEYLRVAPP 1203
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                DEYLTPQQGFF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xiphophorus xiphidium
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Submitted (JUL-2000)
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                                                                                                                - SHPSSCPKCDPSCPNGSCWGGGEBNCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
                                                                                                                                                     ASLSFLQDIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                                                                                                                                                              129 VIGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI
                                                                                                                                                                                                                                                                                                                                             LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE
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                                                                                              11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                                                                                                                                                                                                                                                      185 DINRSRACHPCSPMCKGSRCWGESSEDCQSLTRIVCAGGCA-RCKGPLPTDCCHEQCAAG
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                                                                     Indels
ATP-binding; Receptor; Transferase.
SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
                                        45.3%; Score 3085; DB 11;
llarity 49.5%; Pred. No. 7.2e-224;
Conservative 167; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                 Matches 630;
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1010 EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
                                                                                                                                      1019 ---EPCIPPNGH--------PURENSIALRYISDPTQNALEKDLDGH- 1054
                                                                                                                                                                                                                                                                       1176 GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS 1235
                                                                                                                                                                                      1129 APLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSP
                                                                                                                                                                                                                 -----RYKRIN-ROGS------
                                                                                                        1070 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC
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WEDLINE-99263203; PubMed=10328884;

MEDLINE-99263203; PubMed=10328884;

Distribution of neuregulin-1 (nrg1) and erbB4 transcripts in milestribution of neuregulin-1;

The mbryonic chick hindbrain.";

Mol. Cell. Neurosci. 13:237-258(1999).

RMEL; AF121863; AAD31641.1; -..

RMEL; AF121863; AAD31641.1; -..

RMESP; P11362, 1FGK.

InterPro; IPR000749; EGFR L. domain.

InterPro; IPR00174; Furin-1ike.

InterPro; IPR00145; TVF pkinase.

InterPro; IPR00145; TVF pkinase.

InterPro; IPR00145; TVF pkinase.

RME Mip PF001057; PR111-1ike; 1...

PFam; PF001057; PR111-1ike; 1...

PFam; PF00107; PR0111-1ike; 1...

PFam; PF001075; PR0111-1ike; 1...

PFam; PF00109; PVFKINASE.

PROSITE; PS00107; PROTEIN KINASE ATP; 1...

RR SMART; SM00219; TVFKINASE TYPK; 1...

RR SMART; SM00219; TVFKINASE TYPK; 1...

RR PROSITE; PS00107; PROTEIN KINASE TYPK; 1...

RR PROSITE; PS00109; PROTEIN KINASE TYPK; 1...
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39.2%; Score 2667.5; DB 13; Length 1137;
Best Local Similarity 46.6%; Pred. No. 2.2e-192;
Matches 534; Conservative 172; Mismatches 350; Indels 89; (
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
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                                                              995 SSDD--DVVDADEYLL-----
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                                                                                   Gaps
                                                                                   148;
                                        Length 1165;
                                                                                 Indels
  1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                        Query Match 39.9%; Score 2716; DB 13; Best Local Similarity 45.6%; Pred. No. 5.1e-196; Matches 582; Conservative 162; Mismatches 384;
SEQUENCE
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Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.
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Last annotation update)
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EMBL; AF056116; AAC34391.1; --
HESPP; P11362; 1FGK.

InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk Pkinase.
InterPro; IPR001244; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain; 2.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                         Created)
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MEDLINE=99177347; Pubmed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA
rubripes.";
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                                                                                                                                                                   PRELIMINARY;
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                                                                        AEQCDGRCYGPYVSDCCHRECAGGCSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTF
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LCSSDGCWGPGPDQCLSCKRFIRGRTCIESCNLYDGEFRBFANGSVCMECDPQCEKMEDN
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.5%; Score 2007.5; DB 5; Length 1433; Best Local Similarity 32.6%; Pred. No. 2.2e-142; Matches 473; Conservative 195; Mismatches 389; Indels 395;
                                                                                                                                                                                                   The Control of the Anopheles gambi epidermal growth factor receptor."; "Cloning, expression and localisation of the Anopheles gambi epidermal growth factor receptor."; Submitted (INOV-2000) to the EMBL/GenBank/DDBJ databases. REMBL; AJ301655; CAC35008.1; "REMBL; AJ301655; CAC35008.1; "REMBL; AJ301655; CAC35008.1; "REMBL; AJ301655; PR000495; CYCC heme bind. InterPro; IPR000495; CYCC heme bind. InterPro; IPR00199; Euk pitnase. InterPro; IPR00199; Euk pitnase. RI InterPro; IPR001245; Tyr pkinase. RI InterPro; IPR001245; Tyr pkinase. RP Ffam; PF0010069; pkinase; 1. RP Pfam; PF001009; PKRINASE. RP PF001009; TYRKINASE. RP SMART; SM00261; FU; 7. SMART; SM00261; FU; 7. SMART; SM00219; TYRC; 1. RP PROSITE; PS00109; TYRC; 1. RP PROSITE; PS00109; PROTEIN KINASE DOM; 1. RP PROSITE; PS00109; PROTEIN KINASE TYR; 1. RP PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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NON TER 1 1
SEQUENCE 1433 AA; 159585 MW; E3D9D88967724F07 CRC64;
                                                                                                                                              SEQUENCE FROM N.A. STRAIN=SUA;
                                                                                                      NCBI_TaxID=7165;
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                        PDLSVPONLOVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
                                                                                                                                                                VPWDQLFR-QYIKANSKFIGITELECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
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                                                                                                                                                                                                                                                                                                                                     ARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA
                                                                                                                                                                                                                                                                                                                                                         SCPAGVN-DGEKGLIFKFPNREGHCEPCHQNCTQGCSGPGLNDC---LEAARLTISSGQ
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YIKANSKFIGITE-----LECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE 543
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                                                                          ----SGVKPDLSYMPIWKFPD---
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                                                                                                                                617 SDYVLQEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQDF
                                                                                                                                                  -----ACQPCPINCT-----HSCVDL-----DD-----KGCPAEQ----
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                                   CRVLQGLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP-
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1148 PSTIAETDEYLQPKTRPSIMLPGPSA-------
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                                                                                                                      Euteleostomi;
Homo.
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                                                                                                                                                                                                                    MEDLINE=99415951; PubMed=10485918; Doherry J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.; Doherry J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.; "The HER-2/neu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
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Dobetty J.K., Cilinton G.M., Adelman J.P., Evans A.J., He
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF17761, AAD56009.2; ..
EnterPro; IPR000494; BGFR L domain.
InterPro; IPR00174; Furin-Tike.
Ffam; PF00757; Furin-Tike; 1.
SPART; SM00261; Furin-Like; 1.
SWART; SM00261; Furin-1ike; 1.
SWART; SM00261; Furin-1ike; 1.
SWART; SM00261; Furin-1ike; 1.
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Bus musculus (Mouse).
Musmusculus (Mouse).
Musmusculus (Mouse).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
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Pred. No. 7.2e-133;
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V-erbB protein (Fragment).
                                          Matches 358; Conservative
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                        Similarity
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MEDLINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Vennstrom B., Raynoscheck C.,
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genes with
different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL; S69372; AAC60725.1;
HSSP; P03322; 1A65
                                                                                                                                Gaps
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                                                                                     Length 367;
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxIb=11950;
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                      ll protein.
367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;
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Last annotation update)
                                                                                 Ouery Match 25.6%; Score 1739; DB 11;
Best Local Similarity 88.0%; Pred. No. 5.5e-123;
Matches 323; Conservative 11; Mismatches 33;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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InterPro; IPR004028; Retro M.
InterPro; IPR001245; Tyr pkinase.
EMBL; BC027080; AAH27080.1; -.
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                    Hypothetical
SEQUENCE 36
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POLYPROTEIN.
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                                                                                                                                                 629 NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
                                                                                                                                                                    748 IPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLL
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MEDLINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Vennstrom A., Beug H.;
Vennstron A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genes with
different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL: S69372; AACG0727.1; -.
                                                                           PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
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25.3%; Score 1720; DB 15; Length 729; 54.8%; Pred. No. 4.2e-121; ive 75; Mismatches 118; Indels 102;
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBI_TaxID=11950;
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LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
"Six amino acids from the retroviral gene gag greatly enhance the
transforming potential of the oncogene v-erb-B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C retroviruses
                                                 A Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T..
A Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T..
A Man D.F., Gu J.R.;
T "Novel human cond clones with function of inhibiting cancer cell:
T "Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
It Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF118349; AAL55856.1; -..
R InterPro; IPR001245; Tyr_Dkinase.
R InterPro; IPR001245; Tyr_Dkinase; I.
R Pfam; PF000061; EWL, pkinase; I.
R ProDom; PD000001; EWL, pkinase; I.
SWART; SM00219; TyrKc; I.
DR RROSITE; PS00011; PROTEIN_KINASE_DOM; I.
HANDELLE PROSITE; PS00011; PROTEIN_KINASE_DOM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%; Score 1697.5; DB 4; Length
80.5%; Pred. No. 9e-120;
ive 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypotherical protein. SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            064895 PRELIMINARY; PRT; 962 AA.
064895;
101-NOV-1996 (TrEMBLrel. 01, Created)
101-NOV-1996 (TrEMBLrel. 01, Last sequence update)
101-NOV-1996 (TrEMBLrel. 21, Last annotation update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
103, v-erb-A, v-erb-B protein.
104, v-erb-A, v-erb-B protein.
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Matches 330; Conservative
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              NCBI_TaxID=9606;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
                                                                                                                                                                                                                                                                                                                                                                                                                     DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697 VEPLTPSGAMPNOAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          877 YHADGGKVPIKMMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1056 GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                            Query Match 25.2%; Score 1718; DB 15; Length 567; Best Local Similarity 55.4%; Pred. No. 4.1e-121; Matches 357; Conservative 73; Mismatches 112; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAKTLSPGKNGVVKDVF------AFGGAVENPEYL 1197
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                                                                                                                                                                                                                                                567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
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InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
ProDom: PD000001; Euk_pkinase; I.
SMART; SM00219; TyrKC; I.
PROSTIE; PS00107; PROTEIN KINASE_DOM; I.
PROSTIE; PS00109; PROTEIN KINASE_DOM; I.
PROSTIE; PS00109; PROTEIN KINASE_TYR; I.
Tyrogine-protein kinase.
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1107 SPLORYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88217326; PubMed=2897102; Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.; Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.; "Common site of mutation in the erbB gene of avian erythroblastosis virus mutants that are temperature sensitive for transformation."; Oncogene Res. 1.265-278(1987).
EMBL; X06943; CAA30024.1; -
HSSP; P11362; IFGK.
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InterPro; IPR001245; Tyr_pkinase.
Fram; PF00069; pkinase; 1.
Pr0000m; PD000001; Euk pkinase; 1.
SWART; SW00129; Tyrkc; 1.
PROSITE; PS00107; PROTEIN KINASE DOP; 1.
PROSITE; PS00109; PROTEIN KINASE DOP; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 545 AA; 60899 MW; 140DCEBCCA0F8AF4 CRC64;
                                                                                                                                                                                                                                                                                                               Q85468;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (T834) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type (NCBI_TaxID=11861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
24.2%; Score 1645; DB 15;
Best Local Similarity 54.9%; Pred. No. 1.3e-115;
Matches 345; Conservative 70; Mismatches 121;
                                                                                                                        -LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
                                                                                                                                                      SINTERPROPERTY SHIP STANDARD S
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                                                                                                                                                                                                                                                                                             PRT;
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085468
AC 08546
AC 08546
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DT NI-NO
DE Avian
OC Virus
COS NOBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

24.3%; Score 1653.5; DB 15; Length 962;
Best Local Similarity 51.7%; Pred. No. 6.7e-116;
Matches 358; Conservative 73; Mismatches 142; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R PRINTS; PR00399; STRDHOENGER.
R PRINTS; PR00147; STROIDFINGER.
R Probom; PD0000015; Euk_pkinase; 1.
R Probom; PD0000015; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00430; TyrKc; 1.
R SMART; SM00399; ZnF_C4; 1.
R SMART; SM00399; ZnF_C4; 1.
R PROSITE; PS000107; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.
R PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.
M ATP-binding; DNA-binding; Nuclear protein; Receptor;
M Transcription regulation; Transferase; Tyrosine-protein kinase;
Oncogene 5:15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 VEECRVLQGLPRE-YVNAR-HCLP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
                                                             EMBL; X52209; CAA36459.1; Che NOLLEAN IN EMBL; X52211; CAA36459.1; Chest in the North interpro; IPRO00719; Euk pkinase. Interpro; IPRO00719; Euk pkinase. Interpro; IPRO01723; Stdhrmn_receptor. Interpro; IPRO01723; Stdhrmn_receptor. Interpro; IPRO01245; Tyr pkinase. Interpro; IPRO01628; Znf_C4steroid. Pfam; PF001094; Pormone_rec; 1. Pfam; PF001094; Pormone_rec; 1. Pfam; PF00105; zf-C4; 1.
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15;

Gaps

92;

969

seq4-465-479-12.rspt

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Search completed: July 22, 2003, 09:01:22
Job time : 53.3575 secs
          "Functional
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STRAIN-C57BL/63; TISSUE-LIVER;

KARAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Staburner M., Batalov S., Casavant T.,

Ruell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Blownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

K., Wannertein M.J., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                         APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1110
                                                                                                                                                                                                          1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1169
                                                                                                                                                                                                                                                        -------PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQIQIYNYISLTAISK 523
                                                                                                                                       SEQUENCE FROM N.A. STRAIN-C3H/101, 129/SVJ, AND 129/SVFVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J. Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maihle N.J.;
"Alternative Transcripts from the Human and Mouse EGFR Genes Encode
Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                            LPMDSRYQN-----SHSTAVDNPEYL 544
                                                                                                      GGDLTLGLEPSEEEAPRSPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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Q9WVFS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                             21.7%; Score 1476.5; DB 11; Lengt llarity 43.9%; Pred. No. 8.8e-103; Conservative 97; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                       72906 MW; 6B34063B1BC928CB CRC64;
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EMBL; AKO04911; BABZ300...

A MGD; MG1:95294; EGFR L domain.

R InterPro; IPR00194; EGFR L domain.

DR Pfam; PF00757; Furin-11ke; 1

DR Pfam; PF01030; Recep L domain; 2.

SMART; SM00261; FU; 3.
                                          EMBL, AF124513; AAD44149.1; --
EMBL, AF275366; AAG28047.1; --
EMBL, AF275364; AAG28047.1; JOINED.
EMBL, AF275365; AAG28047.1; JOINED.
EMBL, AK07444; BAB23681.1; --
EMBL, AK004883; BAB23641.1; --
EMBL, AK004881; BAB23641.1; --
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HER2 transgene pla
HUman HER2 (ErbB2)
HUman HER-2/neu pr
Human HER-2/neu pr
Amino acid sequenc
Human HER-2/neu pr
Human HER-2/neu pr
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1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAB60167
AAW014111
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AAW921198
AAY84780
AAB85158
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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|Jabel= insertion_region
|note= "sultable For Foreign epitope insertion"
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|abel= insertion_region
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/label= insertion region
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                                                                                                                                                                                                                                                                                        Tyrosine_kinase_domain
                                                                      Ligand binding domain
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|label= Transmembrane_domain
label= Cysteine_rich_domain
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|Tabel= C-terminal_domain
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/label= Ty:
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/label= L
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/label= C
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-procedins). e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 80 (FGR8D). The method comprises effecting simultaneous presentation by antigen producing cells (APCRS) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 blist T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGR8D comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least to foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer
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                                                                                                                                                                                                                                                                                                                                           when the PA is human PSM, FGF8b and Her2, respectively.
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful cor inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines can to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host calls. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and 9185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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16-MAR-2000; 2000US-0189844.
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N-PSDB; AAF24297.
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is characterised by the overexpression of an epidermal growth factor with an anti-ErbB and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody comprising administering to the mammal an anti-ErbB antibody maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomed, endomerrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbBz. The method is also useful for treating neuronal, glial, strond, hypothalamic, glandular, macrophagal, immunological disorders. This sequence represents the human HER2 (ErbBz) polypeptide of the invention.
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SLIWKOWSKI M.
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                                      HQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1DVYMIMVKCWM
                                                                    NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
        LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRFT
                                                           IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                          EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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                              HQSDVWSYGVTVWELMTFGAKPYDG1PARE1PDLLEKGERLPQPP1CT1
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malignancy; treatment; tumour.
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676..1255
/note= "region which
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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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           AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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EEYLVPQQGFFCPDPAPGAGGWVHRRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                       AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                               NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                           GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                                                                                 The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as archropathy, bone resorption, inflammatory diseases, degenerative disorders of the
                                EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                              SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
                                                                                                                                                                                                                                                                                          Amino acid seguence of the SPLICE erbB-2 receptor protein.
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                                                                                               MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                             ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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 Score 6631;
Pred. No. 0;
97.5%;
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NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVPAFGGAVENDEYLTPQ 1200
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NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVPAFGGAVENPEYLTPQ
                                                                                                                                              Antigen-presenting cell; immunogenic; immune response; HER-2/neu; oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes isolated prepared HER2/neu epitopes (I).

Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is

culture in vitro and binds to a complex of an epitope (I), bound to a

channal leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)

and a second epitope and the peptide is less than 50 contiguous amino

ccids that have 100% identity with a native peptide sequence of HER2/neu;

(3) a vaccine composition (II) comprising (II) and a pharmaceutical

cc excipient; (4) an isolated nucleic acid encoding a peptide comprising

(1); and (5) and (11) are useful for inducing cellular immune responses for the

prevention and treatment of cancer. (I) and (II) are useful for

cm (III) are useful for inducing cellular immune responses for the

prevention and treatment of cancer. (I) and (II) are useful for

cm onitoring or evaluating an immune response to a tumour-associated

antigen when incubated with a T lymphocyte sample form a patient and

cc antigen when incubated with a T lymphocyte (I) (II). Epitope

cc antigen mean that immunosuppressive epitopes that may be present

cc in whole antigens may be avoided. Selected epitopes that may be combined to

contain an antigen and antigen antigen and antigen 
1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Byltope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-immunation ariability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent amino acid sequences used it the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                      Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
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cellular immune responses for the prevention and treatment of cancer
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 EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                       AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                                                                                                                                                                            Human, Her-2, epidermal growth factor receptor 2; infection; cancer;
hyperproliferative disorder; prophylaxis; inflammation; antisense;
tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is buman leukocyte antiquen (HLA)-844 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of preferably breast cancer, in pharmaceutical compositions, e.g., vaccine of numan malignancies, for stimulating and/or expanding T cells specific for therapy and other compositions for the diagnosis, prevention and treatment of cancer in a patient. The invention is useful for stimulating a T cell response in a patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/New gene fragments of interest, to isolate a full contrained malignamicies and for the treatment of cancer, prophylactic or therapputations and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/New.
epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated Her-2/Neu polypeptide composition
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                                      GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated Her-2/Neu polypeptide composition useful for therapy prevention and diagnosis of cancer, preferably breast cancer
                                                    GGAAPOPHPPPAFSPAFDNLYYWDODPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                                                            Human; Her-2/Neu protein; immune response; gene therapy; breast human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
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                                     AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                     NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                       AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                   GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                                                                                                                                                                                                                                                                                                Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
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comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of a her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ax vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in corder to inhibit the development of cancer in a patient.
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Zhneu or a polymuclectide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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6; Mismatches
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                                                                                        YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
           IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
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28-SEP-2000; 2000US-0675904.
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Search completed: July 22, 2003, 08:41:34 Job time: 42.9774 secs

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July 22, 2003, 08:12:49; Search time 10.2304 Seconds (without alignments) 5088.033 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                               OM protein - protein search, using sw model
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SEQ4-465-479-12 6804 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 112892 segs, 41476328 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Perfect score: Scoring table: Sequence: Searched: Title:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

P54760 homo sapien	Q07494 gallus gall	Q91736 xenopus lae	Q91571 xenopus lae	P07949 homo sapien	Q03145 mus musculu	P54761 mus musculu	P29317 homo sapien	Q00944 gallus gall	P53356 hydra atten	O91738 xenopus lae	P34152 mus musculu	
EPB4 HUMAN	EPB1 CHICK	EPBB_XENLA	EPBA_XENLA	RET HUMAN	EPAZ MOUSE	EPB4 MOUSE	EPA2 HUMAN	FAK1 CHICK	HT16 HYDAT	FAK1 XENLA	FAK1_MOUSE	
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603	601.5	593	587.5	587	585.5	585	584.5	578.5	573	269	565.5	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT ERB2_HI ID_EI	ERB2_HUMAN BERD_HUMAN BERD_ERB2_HUMAN STANDARD; PRT; 1255 AA.
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\$	Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
\$ £	Saito T., Toyoshima K.; "Similarity of protein encoded by the human c-erb-R-2 gene to
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Z Z	Nature 319:230-234(1986). [2]
RP	SEQUENCE FROM N.A.
%	MEDLINE=86070181; PubMed=2999974;
8 8	Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., McGrath J., Seeburg D.H., Libermann T.A., Schlessinger J.
2	Francke U., Levinson A., Ullrich A.;
RT	"Tyrosine kinase receptor with extensive homology to EGF receptor
R.	<pre>shares chromosomal location with new oncogene."; Science 230.1132-1139(1985)</pre>
2	[3]
8 c	SEQUENCE OF 737-1031 FROM N.A.
2 2	MEDDINESCOLO/29; PUDMEG=299596/; Semba K Kamata N Movochima K Vamamoto H .
ξ. Έ	orotooncogene, c-erbB-2, is distinct
RT	Jene
Z Z	numan salivary giand adenocarcinoma."; Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985)
2	[4]
8. 2.	VARIANTS VAL-654 AND VAL-655.
≨ \$	Ebsani A., Low J., Wallace R.B., Wu A.M.:
RT	"Characterization of a new allele of the human ERBB2 gene by allele-
Z Z	<pre>Specific competition hybridization."; Genomics 15:406-409(1993)</pre>
ខ្ល	TON: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR
98	ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A DOTENTIAL LICAND EOD THIS BECEDAND NOT ACTIVATED BY ECF TOE.
ខ	AMPHIREGULIN.
ខ្ល	
ខ	tyrosine phosphate. -!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
႘	(POTENTIA
ပ္ပ	-!- SUBCELLULAR LOCATION: Type I membrane protein.

rattus norv hydra atten mus musculu homo sapien

cavia porce homo sapien

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MOUSE

DROME HUMAN

EPB1

aedes aegyp

rattus norv homo sapien

drosophila

lymnaea sta

mus musculu

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AAGCTGPKHSDCLACLHFNHSG1CELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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Pred. No. 0;
6; Mismatches 24; Indels 0
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39E9DFDA04DCF962 CRC64;
 BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BP-10 MC GLCNAC.
N-LINKED (GLCNAC...) (PC-10 MC GLCNAC...) (PC-10 MC GLCNAC....) (PC-10 MC GLCNAC...) (PC-10 MC GLCNAC....) (PC-10 MC GLCNAC....) (PC-10 MC GLCNAC.....) (PC-10 MC 
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Best Local Similarity 97.6%;
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMTLARITY).

POLYMORPHISM: THERE AE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-1LE-1LE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-1LE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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EMBL, M1761, AAA35808.1; JOINED.
EMBL, M11762, AAA35808.1; JOINED.
EMBL, M11763, AAA35808.1; JOINED.
EMBL, M11764, AAA35808.1; JOINED.
EMBL, M11765, AAA35808.1; JOINED.
EMBL, M11765, AAA35808.1; JOINED.
EMBL, M11730, AAA35808.1; -...
EMBL, M12036; AAA35978.1; -...
EMBL, X03363; CAA27060.1; -...
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InterPro; IPR002174; FurIn-like.
InterPro; IPR004019; YLP_motif.
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PIR; A24571, A24571.
HSSP, PI1362, IFCK.
Genew; HGNC:3430; ERBB2.
MIM; 164870; -.
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WEDLINE=94193007; PubMed=7908275;

WEDLINE=94193007; PubMed=7908275;

WARAMULTA T., Ushijina T., Ishizaka Y., Nagao M., Arai M.,

Yamazaki Y., Ishikawa T.;

Yamazaki Y., Ishikawa Y.;

Yamazaki Y.
NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mamanlai, Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(pl65erbB2) (NEU proto-oncogene) (C-erbB-2).
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SUBCELLULAR LOCATION: Type I membrane protein.
PITM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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CYSPLASMIC (POTENTIAL).

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ATP (BY SIMILARITY).

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86.0%; Score 5851.5; DB 1; Length 1254;

Query Match

1200

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NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
     EEYLVPQQGFFFFDDPAPGAGSTAHRRHRSSSTRSGGGELTLGMEPSGEEPPRSPLAPSEG 1080
                                   AGSDVFDGDLGMGAAKGLOSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                  GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                                                                           PRT; 1257 AA
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TISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TAXID=10116;
                                                                                                                                                                   STANDARD;
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                                                                     ELTYLPTNASLSFLODIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                             DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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       ed. No. 2.8e-305;
Mismatches 114;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ TISSUE=Neuroblastoma;
MEDILIDE=86118662; PubMed=3945311;
Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal growth factor receptor-related proto. LYFOSINE PHOSPHATE.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER FORMS A HOMODIMER.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY. 01-JAN-1988 (Rel. 06, Created)
15-DESC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p185srbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor ERBB2 OR NEU. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus Lai C., Lemke G.; "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991). MEDLINE=92155181; PubMed=1346763; MEDLINE=92155181; PubMed=1346763; MEDLINE=92155181]; PubMed=1346763; MEDLINE=92155181]; PubMed=1346763; MEDLINE=92155181]; PubMed=1346763; MEDLINE=92155181. Mulvey D., Sternberg M.J.E., Campbell I.D.; Three dimensional structure of the transmembrane region of the prooncogenic and oncogenic forms of the neu protein."; and oncogenic forms of the neu protein."; II.43-48(1992).

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

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ELTYLPTNASLSFLQDIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
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ROTTEIN KINASE.
ATP (BY SIMILARITY).
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SWART; SM00261; FU; 3.
SWART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TyR; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprocean; Multigene family; Receptor; Signal; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; SignAL.
SIGNAL.

1 21 POTENTIAL.
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• E (IN ONCOGENIC NEU).
6129264583011402 CRC64;
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Pred. No. 3.4e-305;
1; Mismatches 120;
 to license@isb-sib.ch)
                                            HSSP, P11362, 1FGK.

INCEPPO, IPR000494; EGFR L domain.
INCEPPO, IPR000119; EUK PKINASE.
INCEPPO; IPR0001174; Purin-like.
INCEPPO; IPR001245; Tyr pkinase.
INCEPPO; IPR04019; YLP motif.
Pfam; PF00069; pkinase; I.
Pfam; PF00157; Furin-like; I.
Pfam; PF00157; Furin-like; I.
Pfam; PF00157; YLP; Z.
            EMBL; X03362; CAA27059.1; ALT INIT.
PIR; A24562; TVRINU.
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120 180 239 240 299 300 359 360 419 420 479 480 538 540 598 900 658 9 718 778 780 840 720 838 898 900 958 PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQY1KANSKF1G1 CAAGCTGPRHSDCLACLHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASCVTTC 421 RDLSVFQNLRIIRGRILHDGAYSLTLQGLGIHSLGLRSLRELGSGLALIHRNAHLCFVHT VPWDQLFRNPHQALLHSGNRPEEDLCVSSGLVCNSLCAHGHCWGPGPTQCVNCSHFLRGQ DPLNNTTPVT-GASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQ CAAGCTGPKHSDCLACLHFNHSG1CELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC TELEFAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL 361 NVQEFDGCKKIFGSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYLYISAWPDSL PDLSVFQNLQVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT VPWDQLFRQY1KANSKF1G1TELE-CVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ **ECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVA** RCPSGVKPDLSYMP1WKFPDEEGACQPCP1NCTHSCVDLDDKGCPAEQRASPLTS1VSAV VGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNOAQMRILKET ELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEI LDEAYVMAGVG FTHQSDVWSYGVTVWELMTFGAKPYDGIPARRIPDLLEKGERLPQPPICTIDVYMIMVKC WMIDSECRPRFRELVSEFSRMARDPORFVVIONEDLGPASPLDSTFYRSLLEDDDMGDLV WMIDSECRPRFRELVSEFSRMARDPQRFVVIONEDLGPSSPMDSTFYRSLLEDDDMGDLV DAREYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPS EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPE 1021 1079 1081 ઠ

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YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLT 1198
             PQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=84219729; PubMed=6328312;
Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.,
"Human epidermal growth factor receptor CDNA sequence and aberrant
expression of the amplified gene in A431 epidermoid carcinoma cells.",
                                                                                                                                 EGFR HUMAN STANDARD; PRT; 1210 AA.
P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732; O00688; Q99222; Q942C9; Q9GXX1; Q9H3C9; Q910688; Q99222; Q9H2C9; Q9GXX1; Q9H3C9; Q1-UUL-1986 (Rel. 01, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor EGFR OR ERBB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDINE=21100872; PubMed=11161793;
REDIOR J.L., Threadgill D.M., Eley G.D., Strunk K.E., Danielsen A.,
Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.)
Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Protein (TEGFR) in ovarian cancer.";
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Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
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MEDLINE=95382957; PubMed=7654368;
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MEDLINE=85270418; PubMed=2991899; Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.; "Characterization and sequence of the promoter region of the human epidermal growth factor receptor gene."; Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
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Evans R.M., Gill G.N., Rosenfeld M.G.;
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Biochem. Biophys. Res. Commun. 124:125-132(1984).
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MEDILME=85046483; PubMed=6093780;
Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
O'Malley B.W.;
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MEDLINE=84245835; PubMed=6330563;
Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma I.Roe B.A., Merlino G.T., Pastan I.;
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J. Biol. Chem. 266:1746-1753(1991).
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Submitted (SEP-1997) to the SWISS-PROT
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                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=98225196; PubMed=9556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. -:- FUNCTION: Isoform 2/truncated isoform may act as an antagonist. -:- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                               Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.; "Characterization of the N-oligosaccharides attached to the atypical Asn-X-Cys sequence of recombinant human epidermal growth factor
                                         Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F., "Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster ovary fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 truncated isoform/TEGFR, 3/p110 and 4, are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphate. SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
   ASN-444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1210;
                                                                                                                                       ASN-352; ASN-361; ASN-568
                                                                                                                                                                                                                                                                                                                                                                                                                "Receptors for epidermal growth factor and other polypeptide
   ASN-175; ASN-413;
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Pred. No. 2.4e-159;
3; Mismatches 356;
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 SITES ASN-128;
                                                                                                                                       CARBOHYDRATE-LINKAGE SITES ASN-56;
                                                                                                                                                      ASN-603.
MEDLINE=20198209; PubMed=10731668;
                              MEDLINE=96398132; PubMed=8962717;
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                                                                                                         Growth Factors 13:121-132(1996)
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 CARBOHYDRATE-LINKAGE
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                                                                                                                  SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGP
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NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TP 1199
              Eisinger D.C., Serrero G.;
Submatted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRANIB-BALB/C, and CD-1; TISSUE-Liver, and Decidua;
STRANIB-BALB/C, and CD-1; TISSUE-Liver, and Decidua;
MEDLINE-93126380; PubMed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=91232866; PubMed=2030916;
Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
"Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C; TISSUB=Liver; MEDLINE=93026370; PubMed=1408137; Advid A., Skorecki K., Yayon A., Givol D.; Promoter region of the murine fibroblast growth factor receptor 2 (bek/KGFR) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The mouse waved-2 phenotype results from a point mutation in the receptor tyrosine kinase.";
                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
STRAIN=B6/T10986: PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=BALBA/C; TISSUE=Liver;
Hibbs M.L.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                           ----DP
                                                                                                                                                             PRT; 1210 AA
                                          QGGAAPQPHPPPAFSPAFDNLYYWDQ-
                                                                                                                                                                                   (Rel. 33, Created)
(Rel. 33, Last seq
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                                                                                                                                                                                                                                                                                                                                                   (bek/KGFR) gene.";
Oncogene 7:1957-1962(1992).
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Oncogene 6:673-676(1991).
                                                                                                                                                             STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
tyrosine phosphate.
SUBCELULUAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA SUMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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R InterPro; IPR000494; Egfr. L domain.

R InterPro; IPR000199; Euk phinase.

R InterPro; IPR000174; Furin-like.

R InterPro; IPR001274; Furin-like.

R Pfam; PF00169; pkinase; 1.

R Pfam; PF00169; pkinase; 1.

R Pfam; PF001001; Euk pkinase; 1.

R Pfam; PF001001; Euk pkinase; 1.

R PRAFT; SM00219; Tyrkc; 1.

R R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R Transmembrane; Glycoprotein; Receptor; Signal; Transferase;

Tyrongene-protein kinase; ATP-binding; Phosphorylation; Repeat.
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EPIDBEMAL GROWTH FACTOR RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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APPROXIMATE.
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EMBL, U03425; AAA17899.1; -.
EMBL, X5968; CAA42219.1; -.
EMBL, L06864; AAA53029.1; -.
EMBL, Z12608; CAA78249.1; -.
HSSP; P11362; 1FGK.
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EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
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 996 QSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCMMI
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TISSUE-Breast carcinoma;
MEDLINE-93189574; PubMed-3183326;
Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G.W.,
Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HER4/P180erbB4, a fourth member of the
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                    TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP----PERGAPPSTFKGTP
                                                                                   VHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTH
                                                                                                                                 QSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific tissue distribution and differential processing in response to phorbol ester.";
J. Biol. Chem. 272:26761-26768(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
(pl80erbB4) (Tyrosine kinase-type cell surface receptor HER4).
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Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
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 (AUTO-) (BY SIMILARITY)
(AUTO-) (BY SIMILARITY)
(AUTO-, MAJOR SITE)
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         ; DB 1;
1.1e-157;
  PHOSPHORYLATION
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49.5%; Pred. No. 1.
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VICTORING Phosphate.
--- SUBUNIT: ACCOUNTING THE A PLOCETH LYLOSHINE = ALLY + PLOCETH
--- SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
RECEPTORS (POTEWITAL).
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESED BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
--- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CEREBELLUM, PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GLAND, AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RICEPPO: IPRO00194; EUK_DAINED.

RICEPPO: IPRO00119; EUK_DAINED.

RICEPPO: IPRO00114; FURIN-11ke.

RICEPPO: IPRO001245; Tyr_Dkinase.

RICEPPO: IPRO001245; Tyr_Dkinase.

RICEPPO: IPRO001245; Tyr_Dkinase.

RICEPPO: IPRO001245; Tyr_Dkinase.

REAM: PF001069; PKINI-11ke; 1.

REAM: PF001069; PKINI-11ke; 1.

REAM: PF001069; PKINI-11ke; 1.

REAM: PF00107; FULP. 2.

ROBORTE: PRO0107; FULP. 2.

ROBORTE: PRO0109; PROTEIN_KINASE ATP; 1.

ROSITE: PS00107; PROTEIN_KINASE TYR; 1.

RECORDER PROSITE: PS0011; PROTEIN_KINASE DOW; 1.
FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTRACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF. TGF-A, AND AMPHIREGULIN.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR PROTEIN-TYROSINE KINASE ERBB-4. EXTRACELLULAR (POTENTIAL). POTENTIAL.
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CYS-RICH.
CYS-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERBB4.
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DOMAIN
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TRANSNEM 652 675
DOMAIN
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1 89 985
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308 323 BY SIMILARITY. 503 512 BY SIMILARITY. 504 520 BY SIMILARITY. 528 532 BY SIMILARITY. 558 569 BY SIMILARITY. 559 577 BY SIMILARITY. 560 BY SIMILARITY. 570 BY SIMILARITY. 580 589 BY SIMILARITY. 580 589 BY SIMILARITY. 580 589 BY SIMILARITY. 591 614 BY SIMILARITY. 593 614 BY SIMILARITY. 594 614 BY SIMILARITY. 595 577 BY SIMILARITY. 596 615 BY SIMILARITY. 597 BY SIMILARITY. 598 BY SIMILARITY. 599 BY SIMILARITY. 590 614 BY SIMILARITY. 591 615 BY SIMILARITY. 592 616 BY SIMILARITY. 593 BY SIMILARITY. 594 BY SIMILARITY. 595 BY SIMILARITY. 596 BY SIMILARITY. 597 BY SIMILARITY. 598 BY SIMILARITY. 599 BY SIMILARITY. 590 BY SIMILARITY. 59	43.3%; Score 2943.5; DB 1; Length 1308; larity 45.2%; Pred. No. 6.2e-150; Conservative 181; Mismatches 377; Indels 183; Gaps	MGLLIALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGQVVQGNLELTY	PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLORLRIVRGTQLFEDNYALAVLDNGDPLN 	NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLI 	AACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG	CTGPKHSDCLACLHFNHSGICELHCPALVIYNTDTFESMPNPEGRYTFGASCVTACPYNY :	STDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE: - UDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQTVDSSNIDK	AGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFBTLEEITGYLYISAWPDSLPDLS	FONLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD 4 	RQXIKANSKFIGITELECVGEGLACHQLCARGHCWGPGPTQCVNCSQPLRGO	VEECRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVACAHYKDPPFCV 5
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531 ICIESCNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGPGPDNCTKCSHFKDGPNCV 590
                                    704 APNQAQLRILKETELKRVKVLGSGAFGTVYKGIWVPEGETVKIPVAIKILNETTGPKANV
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RKPVAPHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVE----
                                                                                                                  706 MPNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                               EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPA----FSPAFDNLYYWDQDPPERGA--
                                                                      RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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602956; 0922N7;
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
ERBB4 OR TYRO-2.
                       ARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGC-
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SEQUENCE OF 1031-1198 FROM N.A.

SEQUENCE OF 1031-1198 FROM N.A.

STRAIN=Spraque-Dawley; TISSUE-Spinal cord;

A MEDLINE-97184212; PubMed=9030624;

Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

Expression of neuregulins and their putative receptors, ErbB2 and Texpression of neuregulins and their putative receptors, ErbB2 and Texpression of neuregulins and their putative receptors, I. J. Neurosci. 17:1642-1659(1997).

1. FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-TONG, STATE AND AMPHIREGULING, SPECIFICALLY NATH THESE FACTORS INDUCES CELL DIFFERENCIATION NOT ACTIVATED BY EGF. TGF-A, AND AMPHIREGULIN (BY SIMILARITY).

1. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

1. SUBUNIT: HOMODINER OR HETERODIMER WITH EACH OF THE OTHER ERBB

Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.";
Neuron 6:691-704 (1991).

"Neuregulins promote survival and growth of cardiac myocytes. Persistence of ErbB2 and ErbB4 expression in neonatal and adult ventricular myocytes.";

Marchionni M.A., Kelly R.A.;

Biol. Chem. 273:10261-10269(1998)

SEQUENCE OF 848-901 FROM N.A. TISSUE-Sciatic nerve; MEDLINE-91222560; PubMed=2025425;

RECEPTORS (POTENTIAL).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TRSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000199; EGFR L domain.

BR InterPro; IPR000199; EUK pkinase.

BR InterPro; IPR00174; Furin-like.

BR InterPro; IPR00174; Furin-like.

BR InterPro; IPR001919; YIVE motif.

BR InterPro; IPR004019; YIVE motif.

BR PRIMIS; PR00109; Pkinase; 1.

BR PRIMIS; PR00109; PKINASE; 1.

BR RIMIS; PR00109; TYRKINASE.

BR RIMIS; PR00101; EUK PKinase; 1.

BR RIMIS; SM00101; EUK PKinase; 1.

BR SMART; SM00101; FU; 4.

BROSITE; PS00107; PROTEIN KINASE DOM; 1.

BROSITE; PS00109; PROTEIN KINASE DOM; 1.

BROSITE; PS00109; PROTEIN KINASE TYR; 1.

Transmembrane; Tyrosine-Protein; Multigene family; Receptor; Signal; Transmembrane; Tyrosine-Protein kinase; ATP-binding; Phosphorylation.

Transferase; Tyrosine-Protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR PROTEIN-TYROSINE EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF041838; AAD08899.1; -.
EMBL; US2S31; AAC53051.1; -.
HSSP; P11362; 1FGK.
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Rattus norvegicus (Rat).

SEQUENCE FROM N.A. NCBI_TaxID=10116;

Han X.,

TISSUE-Heart; MEDLINE=9821155; PubMed=9553078; Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J.,

Oy 157 IGITELERAGCKKIFGSLAFLPESFDODPASNTAPLODEGLOVFETLEEITGTLYISAMP 416 Db 349 DSSNINDERTNOTKINGALIANGAYBLTCGLIGBALLREBELGSCLALIHNITHLCF 476 417 DSLPDLSVPGNLOVIGRRILHNGAYBLTCGLIGBALLREBELGSCLALIHNITHLCF 476 417 DSLPDLSVPGNLOVIGRRILHNGAYBLTCGLIGBALLREBELGSCLALIHNITHLCF 476 417 WHYPAPPENTATIOGRALIANGAYBLTLGGLIGBALLREBAGGLACHGLCANGHWGAPGTOCWG 531 469 VHTINWTTLFSTVNGRILYIGANGATICLECVGCAGGLACHGLCANGHWGAPGTOCWG 531 469 YHTINWTTLFSTVNGRILYIGANGATICLECVGCAGGLACHGLCANGCHWGAPGTOCWG 531 521 SQPLRGQBCVBECRULGGLPREYNARHCLPCHPECQP ONGSVTCFGPEADCCACC 523 OY 531 SQPLRGQBCVBECRULGGLPREYNARHCLPCHPECQP ONGSVTCFGPEADCCACC 523 OY 531 KNDPFCVARCESGVKDLSYMPINKFPDEEGACQPCPINCTHGCWGPGPDQCLSC 523 OY 643PABCQARAGTLSTSVANY GLILVYVALCHCHPECQP ONGSVTCFGPEADCTYCGHFF 591 DD 524 RRESRCHCTISSCALYOGERREPRAGGSCVPCGLILTGRACGLITHGRGCWGPFSPDCTYCGHF 641 COY 643PABCQARAGTLAGTSTSVAND GLILVYVALCHWGLILTGRACGLITHGRGCWGPFSPDCTYCGHF 641 COY 644 STIPQHAR - TPLIAACVIGGPTTLVIMALTFAVYVRRKSIK-KRGALRFL-EFTELWE 696 OY 640 PLIPSGAMPNOAQMRILKGTELRKYVLLGGGGGTTVYKGINVPGGRYLIPARILLOFTELW 756 OY 641 STIPQHAR - TPLIAACVIGSPTGTTVKGINVPGGRYLIPARILLOFTELW 756 OY 642 STIPQHAR - TPLIAACVIGSPTGTTVKGINVPGGRYLIPARILLOFTELLOFTEL TO TOTOLARY TRENT 756 OY 643 STIPQHAR - TPLIAACVIGSPTGTTVKGINVPGGRYLIPARILLOFTEL TO TOTOLARY TRENT 756 OY 644 STIPCHAR - TPLIAACVIGSPTGTTVKGINVPGGRYLIPARILLOFTEL TO TOTOLARY TO TOTOLA	QY 998 SPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCDPP
186 334 CYS-RICH. 718 985 ATP (BY SIMILARITY). 724 732 ATP (BY SIMILARITY). 843 843 843 SIMILARITY). 843 843 843 SIMILARITY. 193 225 BY SIMILARITY. 230 239 SIMILARITY. 249 258 BY SIMILARITY. 249 258 BY SIMILARITY. 262 289 BY SIMILARITY. 263 330 BY SIMILARITY. 264 258 BY SIMILARITY. 265 289 BY SIMILARITY. 265 289 BY SIMILARITY. 267 BY SIMILARITY. 268 BY SIMILARITY. 269 BY SIMILARITY. 261 BY SIMILARITY. 262 BY SIMILARITY. 262 BY SIMILARITY. 263 512 BY SIMILARITY. 264 BY SIMILARITY. 265 569 BY SIMILARITY. 266 631 BY SIMILARITY. 267 BY SIMILARITY. 268 BY SIMILARITY. 269 BY SIMILARITY. 261 BY SIMILARITY. 261 BY SIMILARITY. 261 BY SIMILARITY. 262 BY SIMILARITY. 263 BY SIMILARITY. 264 BY SIMILARITY. 265 BY SIMILARITY. 266 BY SIMILARITY. 267 BY SIMILARITY. 268 BY SIMILARITY. 269 BY SIMILARITY. 260 BY SIMILARITY. 261 BY SIMILARITY. 261 BY SIMILARITY. 262 BY SIMILARITY. 263 BY SIMILARITY. 264 BY SIMILARITY. 265 BY SIMILARITY. 265 BY SIMILARITY. 266 BY SIMILARITY. 267 BY SIMILARITY. 268 BY SIMILARITY. 268 BY SIMILARITY. 269 BY SIMILARITY. 260 BY SIMILARITY. 260 BY SIMILARITY. 261 BY SIMILARITY. 262 BY SIMILARITY. 263 BY SIMILARITY. 264 BY SIMILARITY. 265 BY SIMILARITY. 266 BY SIMILARITY. 267 BY SIMILARITY. 268 BY SIMILARITY. 268 BY SIMILARITY. 269 BY SIMILARITY. 260 BY SIMILARITY. 260 BY SIMILARITY. 260 BY SIMILARITY. 261 BY SIMILARITY. 262 BY SIMILARITY. 263 BY SIMILARITY. 264 BY SIMILARITY. 265 BY SIMILARITY. 266 BY SIMILARITY. 267 BY SIMILARITY. 268 BY SIMILARITY. 269 BY SIMILARITY. 260 BY SIMI	Query Match 42.9%; Score 2921; DB 1; Length 1308; Best Local Similarity 44.0%; Pred. No. 9.9e-149; Best Local Similarity 40.0%; Pred. No. 9.9e-149; Best Local Similarity 41.0%; Pred. No. 9.9e-149; Best Local Similarity 41.0%; Pred. No. 9.9e-149; Best Local Similarity 41.0%; Pred. Pred. No. 9.9e-149; Best KKCPHNFV-VDSSSCVRACPSSRMEV-EENGIRMCKPCTDICPRACDGIGTGSLMSAQTV 348

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
01-JAN-1990 (Rel. 13, Created)
LoCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112).
                                                                                                         Xiphophorus maculatus (Southern platyfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Cyprinodontiformes, Poeciliidae, Xiphophorus.
                                                                                                                                                                                                                                                           MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
-! SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGHENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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ATP (BY SIMILARITY).
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HSSP; P11362; 1FGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk Dkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002194; Furin-like.
InterPro; IPR001245; Tyr_Dkinase.
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LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1076
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                                              ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAG
                                                                                                                      VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoutation update)
15-GED protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
Homo sapiens (Human).
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P21860;
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                                                                                                                                                                                                                                                                                                                                                               SECRETED (SHORT FORM).

-!- ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
-!- DOMAIN: THE CYTOPLASNIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH1 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSCIATION WITH THE PRES SUBUNIT OF PHOSPHATIDYLINGSITCL 3-KINASE (BY SIMILARITY).
-!- DISEASE: OVEREXERSEED IN A SUBSET OF HUMAN MAWMARY TUMORS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR000199; EGFR L domain.

B. InterPro: IPR000199; Euk pkinase.

B. InterPro: IPR0001245; FurIn-like.

DR InterPro: IPR0001245; Tyr pkinase.

DR InterPro: IPR001245; Tyr pkinase.

DR Ffam; PF00130; Recep L domain; 2.

DR Pfam; PF00130; Recep L domain; 2.

DR Pfam; PF00130; Recep L domain; 2.

DR ProDom; P000001; Euk pkinase; 1.

DR SWART; SW00219; TyrKc; 1.

R SWART; SW00219; TyrKc; 1.

R SWART; SW00219; TyrKc; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; FALSE NEG.

R PROSITE; PS00119; PROTEIN KINASE DOM; 1.

W Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;

W Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

M Alternative splicing.

T SIGNAL
Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3. EXTRACELLULAR (POTENTIAL).
                  Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an additional epidermal growth
Eactor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
                                                                                                                                                                                                                                                                                                                                                 -! - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND
                                                                                                                                TISSUE=Placenta;
MEDLINE=932822; PubMed=7685162;
MEDLINE=932822; PubMed=7685162;
MEDLINE=93282822; PubMed=7685162;
"C-exb83 gene encodes secreted as well as transmembrane receptor tyrosine kinase.";
                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                         tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                              SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M29366; AAA35790.1; -.
EMBL; M34309; AAA35979.1; -.
EMBL; S61953; AAB26935.1; -.
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HSSP; P11362; 1FGK.
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166 755 826 886 875 946 935

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                                                                                                                                                                                                                     -SPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAM
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                                DPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA---
                                                                                                                                                                                                                                                                                          PNQAQMRILKETELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKE
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            -----LECVGEGLACHQLCARGHCWGPGPTQCVNC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor
(c-erbB3).
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Pred. No. 1.5e-120;
; Mismatches 445; Indels 155;
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7201E7F66CA374BD CRC64;
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Matches 530; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U29339 AAC38050.1; ...
R EMBL; U29339 AAC38050.1; ...
R EMBL; U52530; AAC33050.1; ...
R EMBL; U52530; AAC33050.1; ...
R INTERPROOF TEROOOD AAC38050.1; ...
R INTERPROOF TEROOOD ACS TO THE EMBL; U52530; AAC38050.1; ...
R INTERPROOF TEROOOD ACS TO THE EMBL; USE TO THE EMBL; PF00063; PALINASE. 1.
R FAUN; PF00063; PALINASE, 1.
R FAUN; PROOF TEROOD ACS TO THE EMBL; THE EMBL; PROOF TEROOD ACS TO THE EMBLY THE EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-:- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.
-:- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.

EXTRACELLULAR (POTENTIAL).
   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                  Koland J.G.
of the
                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
                                                                                                                                                                            [2]
REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Liver;
STRAIN-Sprague-Dawley; TISSUE-Liver;
HEDLINE-S6096535; Pubmed-8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L.,
"Cloning of the rat ErbB3 cDNA and characterization recombinant protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
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Gene 165:279-284(1995)
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SIGNAL 1 19
CHAIN 20 1339
                NCBI_TaxID=10116;
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34.1%; Score 2323.5; DB 1; Length
Best Local Similarity 40.6%; Pred. No. 8.4e-117;
Matches 523; Conservative 173; Mismatches 426; Indels
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SBO RDGPHCVNSCPHGILG--AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEVLM
                                                                                                                      KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC--VDLDDKGCPAEQRA
                                                                                                                                                                               768 LDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCM
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                                                                                                       SPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMP
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Ukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoc
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae, Drosophila.
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hila relative of ERBB)
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P04412; O61601; O9WZG0; P81866;
13-AUG-1997 (Rel. 05, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
Epidermal growth [actor receptor precursor (EC 2.7.1.112)
Gurken receptor) (Torpedo protein) (Drosophila relative of EGFR OR TOP OR C-ERBB OR DER OR CG10079.
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MEDLINE=94350209; Pubmed=8070664;
Clifford R., Schupbach T.;
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NCBI_TaxID=7227;
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RAMELINE-20196006; Bubmed=10731132;
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RAMADINE-20196006; Bubmed=10731132;
RAMADINE-2019606; Bubmed=10731133;
RAMADINE-2019606; Bubmed=1073133;
RAMADINE-2019606; Bubmed=107313;
RAMADINE-2019606; Bubmed=1073;
RAMADINE-2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeBokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING
STRAIN=Oregon-R; TISSUE=Embryo;
MEDLINE=87002474; PubMed=3093080;
                                                                                                                                                                                                       er J., Shilo B.-2
conservation of
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                                                                                          Clifford R., Schupbach T.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                              Schejter E.D., Segal D., Glazer L., Shilo B.-Z., "Alternative 5' exons and tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila EGF receptor homolog transcripts.";
                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE-85124611; PubMed=2982499; Livneh E., Glazer L., Segal D., Schlessinger in Drosophila EGF receptor gene homolog: conhormone binding and kinase domains.";
subdomains of the receptor protein."; Genetics 137:531-550(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM TYPE I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                     Cell 40:599-607(1985).
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                                                                   REVISIONS
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SEQUENCE OF 959-1078 FROM N.A Science 287:2185-2195(2000)

receptor homolog reveals

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF receptor.";

Cell 89:13-16(1997).

-!- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS,
WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAP-
MARK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.
CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE
DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DOSSO-VENTRAL
POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE
ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF ANNIOSEROSA
AND VENTRAL NEUROSCTODERMAL CELLS, GERM BAND RETRACTION, CELL FATE
SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE II; ARE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN INIG DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BEALN CORFEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                        [8]
SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                              Raz E., Schejter E.D., Shilo B.Z.; "Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97248481; Pubmed=9094709;
Perrimon N., Perkins L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                          MEDLINE=85137938; PubMed=2983232; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; A Drosophila genomic sequence with homology to human epidermal growth factor receptor."; Nature 314:178-180(1985).
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EMBL, AF052754; AAC08556.1;

EMBL, AF052754; AAC08535.1;

EMBL, AF052752; AAC08535.1;

EMBL, K03054; AAC08535.1;

EMBL, K0317; AAA51462.1;

EMBL, K03414; AAA51462.1;

EMBL, K03418; AAA51461.1;

EMBL, AF109077; AAD26132.1;

EMBL, AF109078; AAD26132.1;

EMBL, AF109078; AAD26132.1;

EMBL, AF109078; AAD26133.1;

EMBL, AF109079; AAD26130.1;

EMBL, AF109079; AAD26130.1;

EMBL, AF109081; AAD26131.1;

EMBL, AF109081;

EMB
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   STRAIN=Daekwanryeong;
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REVIEW.
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AAD26135.1;

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PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 32.5%; Pred. No. 1.7e-95;
Matches 466; Conservative 187; Mismatches 422; Indels 360; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane, Glycoprotein, Receptor, Phosphorylation, Transferase,
Tyrosine-protein kinase, ATP-binding, Signal, Alternative splicing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1925; DB 1; Length 1426; Pred. No. 1.7e-95;
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EXTRACELLULAR (POTENTIAL)
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                   EMBL; X02293; CAA26157.1; -..
EMBL; X78920; CAA5523.1; -..
EMBL; X78919; CAA55221.1; -..
EMBL; X78919; CAA5522.1; -..
PIR; A00640; QOPPE.
HSSP; P11362; 1FGK.
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32.5%;
AE003454; AAF46732.1;
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CHAIN 31 1426
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ACT SITE
MOD RES
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EAIAKPDDYLOPKAAPGPS-----HRTDCT------DEMPKLNRYCKDPS 1276
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543 RWPAIQKEPECKWWNENLR.---ADL-CEKNGTICSDQCNEDGCWGAGTDQCLTCKNFN 597
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                                      RGOECVEECRVLOGLPREYVNARHCLPCHPECOPONGSVTCFGPEADOCVACAHYKDPPF
                                                                                                                  CVSECPKNKYNDRGVCRECHATCDGCTGPKDTIGIGACTTCNLAIINNDATVKRCLLKDD
                                                                                                                                                          EQCETECPADHYTDEEQRECFQRHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTM
                                                                                                                                                                                                                                                -----CPAEQR------ASPLTS-----IVSAVVGILLVVVLG
                                                                                                                                                                                                                                                                        827 FNCTSKCPLEMRHVNYQYTAIGPYCAASPPRSSKITANLDVNMIFIITGAVLVPTICILC
                                                                                                                                                                                                                                                                                                 VVFGILIKRRQQKIRKYT--MRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVL
                                                                                                                                                                                                                                                                                                                    GSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLL
                                                       -----SC-----NDLDDKG-----
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EMBL; M10066; AAA48763.1; ALT_INIT.

PIR; A00643; TVCHLV.
PIR; B00643; TVCPLLV.
HSSP; P11362; IPGK.
InterPro; IPR00719; Buk pkinase.
InterPro; IPR001245; Tyr pkinase.

LYFOSINE PHOSPHATE.

MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS
IN CHICKE WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS BEEN INDUCED BY
THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE
C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Raines M.A., Kung H.-J.;
"c-erbB activation in ALV-induced erythroblastosis: novel processing and promoter insertion result in expression of amino-truncated EGF receptor.";
Cell 41:719-726(1985).

SEQUENCE FROM N.A. MEDLINE=8522822; PubMed=2988784;

Retroid viruses; Retroviridae; Alpharetrovirus

leukosis virus

Viruses, Retroid NCBI_TaxID=11864;

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118 APNOAHLRILKETEFKKVKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAHFIDGPHCVKACPAGVLGENDT.-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 634;
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79; Mismatches 135; Indels
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E705E33A0BE01FCC CRC64;
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165 AT
257 BY
70891 MW;
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138
165
257
634 AA;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
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634 AA

STANDARD;

ERBB ALV P00534;

GE DT CE

RESULT 12

17; 646

Oncogene;

ATP (BY SIMILARITY).
ATP (BY SIMILARITY). PROTEIN KINASE

Phosphorylation

Glycoprotein;

DOMAIN NP BIND BINDING

PEAM; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; ENk pkinase; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-profein kinase; ATP-binding;

705

825 177

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EMBL; K02006; AAA42394.1; ALT_INIT.
EMBL; K01216; AAA42400.1; -.
                                                                                                                                                                                                              Phosphorylation.
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                                                                                   ICTIDUYMIMUKCWMIDSECRPRFRELVSEFSRWARDPORFUVIQ-NEDLGPASPLDSTF 1004
                                                                                                                                                                                                                                                                               NGVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY 1222
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DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS
IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                  PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
                                                                                                 YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                                                                                                                                                                                                         ----SRIPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQRYSSDPTGN
                                                                                                                                                                                                                                                            -----TAMVQ
                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-152 FROM N.A.
MEDLINE=8423957; PubMed=6328658;
MEDLINE=8423957; PubMed=6328658;
Bebuils B., Henry C. Benaissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erba gene of avian erythroblastosis virus reveals a new type of nocogene.";
Science 224:1456-1459(1984).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN CHICKENS.
MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-H;
MEDLINE-84026539; PubMed-6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima J
"The erbB gene of avian erythroblastosis virus is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112) V-ERBB.
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Viruses; Retroid viruses; Retroviridae; Avian type C
NCBI_TaxID=79685;
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21-JUL-1986 (Rel. 01, Last seq
15-JUN-2002 (Rel. 41, Last ann
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Cell 35:71-78(1983).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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52.2%; Pred. No. 4.7e-84;
ive 76; Mismatches 128; Indels 126; Gaps
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HSSP, P1162; 1FGK.
InterPro; 1PR000719; Euk_pkinase.
InterPro; 1PR000719; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
Pr000m; P000001; Euk_pkinase; 1.
Pr050m; P00019; Tyrkc; 1.
PROSTTE; PS00109; PROTEIN KINASE ATP; 1.
PROSTTE; PS50010; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
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138 146 ATP (BY SIMILARITY).

165 165 ATP (BY SIMILARITY).

29 29 R -> W (IN REF. 2).

140 140 S -> F (IN REF. 2).

146 146 I -> V (IN REF. 2).

604 AA; 67633 MW; 76EBCDD06745D609 CRC64;
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885 297 945

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1065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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   APNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELREATSPKANK 177
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                                                                                           CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                                                     IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SÜBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to
MISCELLANEOUS: Binding of EGF to the EGF-receptor complex,
inderization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     ----SRIPLLSSLSATSNNSATNCIDRNGG------H-----H
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01-JNN-1990 (Rel. 13, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112)
(Fragment).
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   ---NTNOSPLAKTVFE 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  706 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                 Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbs confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKPPDEEGACOPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                         Avian erythroblastosis virus (strain ta167).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=103898;
                                                                                                                                                               01.JUL-1989 (Rel. 11, Created)
01.JUL-1989 (Rel. 11, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                             . Cell. Biol. 6:1751-1759(1986).
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; TYPKC. 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein_Kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.0%; Score 1630; DB 1; Length 540; 55.1%; Pred. No. 3.3e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H -> D (IN THERMOLABILE V-ERBB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5B53297AA068B65D CRC64;
 ---VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                             NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1248
                                                           594
                                                                                                                                    540 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                        SSPYWIQSGNHQ-----INLDNPDY
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                   MEDLINE=87064458; PubMed=2878364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M13179; AAA42401.1; -. PIR; A25231; TVFVEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.1%
Matches 341; Conservative
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                  EPIDERMAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.1%; Score 1575; DB 1; Length 703; larity 44.2%; Pred. No. 3.8e-77; Conservative 111; Mismatches 254; Indels 3
                                                                                                                                                                                                                                                                                                                                            Signal; Transferase;
                                                                                                                                                                                                                                                       SMART; SM00261; FU; 4.

PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.

PROSITE; PS00109; PROTEIN KINASE TYR; PARTIAL.

PROSITE; PS50011; PROTEIN KINASE DOM; PARTIAL.

Transmembrane; Glycoprotein; Receptor; Signal; Transfer

Tyronine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77427 MW; AFF2DE11B735A690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIM
                                                                                                          EMBL. M20386; AAA48760.1; -. Gomain. InterPro; IPR000494; EGFR L domain. InterPro; IPR000719; Euk pkinase. InterPro; IPR0012174; Furin-like. InterPro; IPR001245; Tyr pkinase. Pfam; PF00757; Furin-like; 1. Pfam; PF00130; Recep_L domain; 2.
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                                                                           302
                                                                                                                                                                                                                                                                                                      -MNKTQ------GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PL 182
                                                                                                                                                                                     419 LPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVH
                                                                                                                                                                                                              TVPWDQLFRQYIKANSKFIGITELECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                                                                                                                                                                                             ECVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHYKDPPF
                                                                                                                                                                                                                                                                CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
                                                                                              PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQY1KANSKF1G1
                                                                                                                                    TELE-FAGCKKI FGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDS
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Search completed: July 22, 2003, 08:46:30 Job time : 20.2304 secs

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July 22, 2003, 08:11:38 ; Search time 37.9774 Seconds (without alignments) 4403.399 Million cell updates/sec
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1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1255
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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ALIGNMENTS

Description	Human herequlin 2	Human tyrosine kin	HER2 transcene nla	Human HER2 (ErbB2)	HER-2/new protein	Human HER-2/nell on	Human HER-2/neu	Amino acid segment	Human HER-2/neu nr	HER2/neu amino aci
ΠD	AAY92620	AAE12130	AAB60167	AAU74545	AAW01111	AAW92406	AAB21198	AAY84780	AAB85458	AAG88267
DB	21	22	22	23	17	20	21	21	22	22
% Query re Match Length DB I	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
% Ouery Match	7.76	7.76	7.76	7.76	97.6	97.6	97.6	97.6	97.6	97.6
Score	6639	6659	6639	6699	6653	6653	6653	6653	6653	6653
Result No.	-	7	æ	4	Ŋ	9	7	80	6	10

Human Her-2 protei	-2/	Her-2/neu	Human Her-2/neu po	ce of c-er	ם '	- 63		Her-2/neu	Mouse Her-2/neu pr	acid seque	Her-		nen		Her-	HER-	Her-2/neu extracel	Her2-GM-CSF immuno	Extracellular HER-	Human Her-2/neu on		Human ErbB2 extrac	DC8scFv-erbB2EC fu	Extracellular port	Amino acid sequenc	Human EGF receptor	Human Her-1 protei	Human epidermal gr	Amino acid sequenc	Human protein for			Human protein for	Human epidermal gr
AAE24067	AAE20479	AAM51143	AAU77114	AAR39568	AAU98923	AAB21208	AAB21199	AAM51144	AAB21206	AAG62860	AAM51151	AAB21203	AAM51148	AAM51152	AAM51153	AAB21204	AAM51149	AAW19764	AAB21200	AAM51145	AAB60408	AAB61593	AAY44993	AAR08222	AAB19259	AAY50616	AAE23019	AAM50768	AAB68420	AAE20483	AAE20481		AAE20482	ABP51768
23	23	23	23	14	23	21	21	23	21	22	23	21	23	23	23	21	23	18	21	23	22	22	21	11	51	23	23	23	22	23	23	23	23	23
1255	1255	1255	1255	1433	1223	1200	1256	1256	1256	1256	1256	919	919	920	926	712	712	782	653	653	645	645	951	624	21	1210	21	21	1210	583	587	589	0	1210
97.6	91.6	97.6	97.6	97.1	95.2	93.0	86.1	86.1	85.8	85.8	85.8	69.5	69.5	58.6	58.6	53.2	53.2	51.0	51.0	51.0	50.4	50.4	49.5	œ.	S.	'n.		45.4	•	•	45.3	Š.	ŝ	44.8
6653	6653	6653	6653	6614	6489	33	869.	869.	846.	5846.5	846.	4739	4739	Ç,	3996.5	3623	3623	3477	3475	3475	3437	3437	3372	3269	3097	3097	3097	3097	3095	3084	3084	3083	3083	3056
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32		34	35	36	37	38	39	40	41			44	45

									T-lymphocyte immunity:	ate cancer:	bitone							=			qn epitope insertion"			qn epitope insertion"			gn epitope insertion"			gn epitope insertion"	
	AAY92620 standard; Protein; 1255 AA.				(first entry)		1 2 (Her2).		12; vaccination; cytotoxic	self-protein; cancer; breast cancer; prostate cancer;	cell-associated peptide antigen: foreign epitope				Location/Qualifiers	1173	/label≈ N-terminal	/note= "mature polypeptide"	525	/label= insertion region	/note= "suitable For forei	5973	/label= insertion_region	/note= "suitable For forei	103117	/label= insertion region	/note= "suitable For forei	149163	/label= insertion_region	/note= "suitable for forei	174323
RESULT 1 AAY92620			AAY92620;		10-AUG-2000		Human herequlin 2 (Her2).						Homo sapiens.			Domain	•		Region			Region			Region			Region			Domain
RES AA	Π	Ž	¥.	ž	Į.	X	DE	×	Š	Ž	Ž	×	SO	ž	Æ	Ŧ	F	E.	F	FŢ	ΕŢ	Η	FJ	FΤ	FI	FŢ	FŢ	ΕŢ	[]	E I	

seq4-369-383-12.rag

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/label= insertion region
/force= "suitable for foreign epitope insertion"
/force= "suitable for foreign epitope insertion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                  124..483
| Tabel = Ligand binding domain
                                                                                                                                                                      184..623
| Jabel = Cysteine_rich_domain
  Cysteine rich domain
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/label= C-terminal_domain
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98US-0105011
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign Thelper epitopes were identified (see features table). The method

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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins).

(PSM), heregulin 2 (Herz) and/or fibroblast growth factor 8b (FGR8b).

The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 or (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Herz and human/murine FGR8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate/preast or breast cancer when the PA is human PSM, FGF8b and Herz, respectively.
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Matches 1227; Conservative
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                     781 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ1AKGMSYLEDVR
                                                                                              LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                                                                                                                                                 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                          LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
774..782
/note= "Antigenic epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tyrosine kinase-type receptor, HER-2
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N-PSDB; AAD19731.
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides inch hose cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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The present invention provides a method of treating cancer by administering a conjugate of anti-BrbB antibody with a maytansinoid. In particular, the antibody is directed against ErbBs (also known as HER2 and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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                                                                                                                                                                                                                                                                                                                                             Human, HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-mayransinoid conjugate; cancer; tumour; breast; ovar stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; pithelial disorder; stromal disorder; stromal disorder; inflammatory disorder; angiogenic disorder; inflammatory disorder;
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
                            EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG
                                                                                                                                        IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                         EEYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                              AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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05-OCT-2000; 2000US-238327P.
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SLIWKOWSKI M.
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N-PSDB; ABK14058.
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is characterised by the overexpression of an epidermal growth factor receptor (BrbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody. Comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, allowage pland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2)
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                  Human HER-2/neu protein (AAM01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The product of ever-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypoptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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                                                                                                                                        HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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                                                                                                                                                                                                                     IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                                                                                        EEYLVPQQGFPCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                            LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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676.1253
/label= Intracellular domain
/note= "claimed domain, useful for immunisation"
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HER-2/neu associated malignancy, particularly for treating or
eventing tumours
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malignancy; treatment; tumou
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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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EEYLVPQQGFFCPDPAPGAGGWHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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                                                                                                                                                                                                                                                                                                                                                                                                                           HER-2/neu, oncogene; tyrosine kinase; cytostatic; vaccine; cancer; prostate cancer; ovarian cancer; lung cancer;
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(SMIK ) SMITHKLINE BEECHAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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Query Match
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                                           DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                            NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                          AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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                                                                                                                                                   GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                 Human HER-2/neu protein.
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The present invention describes isolated prepared HER2/neu epitopes (I).

Also described are: (1) a clonal cytocoxic T lymphocyte (CTL) that is

CC culture in vitro and binds to a complex of an epitope (I), bound to a

human leukocyte antigen (HLA) molecule; (2) a peptide (II) bound to a

conductive in vitro and binds to a complex of an epitope (II) bound to a

conductive in vitro and binds to a complex of an epitope (II) bound to a

conductive composition (III) comprising (II) and a pharmaceutical

conductive composition (III) comprising (II) and a pharmaceutical

conditionaliant activities, and can be used in vaccines (I), (II)

conditionaliant activities, and can be used in vaccines (I), (II)

conditionaliant activities, and can be used in vaccines (I), (II)

conditional and treatment of cancer. (I) and (III) are useful for

conditioning or evaluating an immune response to a tumour-associated

conditioning or evaluating an immune response to a tumour-associated

antigen when incubated with a T lymphocyte sample form a patient and

detecting the presence of bound T lymphocyte sample form a patient and

conditional man that immunosuppressive epitopes that may be present

conditional may be avoided. Selected epitopes may be combined to

conditional antigens may be avoided. Selected epitopes may be combined

conditional antigens from the same pathogen. Epitope-based anti-tumour

conditional provides the opportunity to combine epitopes derived from

multiple tumour-associated molecules addressing the problem of tumour

conditional loss. AAG88266 to AAG89121 represent amino acid sequences used in

the exemplification of the present invention.
1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
                                                                                                                                                                                                                                                                                                                  Human, HER2/neu, epitope, human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated prepared HER2/neu epitope useful in a vaccine for inducincellular immune responses for the prevention and treatment of cancer
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                                                                                                                                                                                                                                                                               HER2/neu amino acid sequence
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                                MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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ive 8; Mismatches
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                                                              YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT
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                                                                                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative diseases or e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                     EEYLVPQQGFFCPDPAPGAGGMVHRRRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                     NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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97.6%; Pred. No. 0;
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Matches 1225;
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The invention relates to an isolated Her-2/Neu polypeptide composition

effective for eliciting an immune response. The invention is useful for

eliciting an immune response. The invention is useful for

eliciting an immune response. The invention is useful for

the composition is useful for the therapy and diagnosis of cancer.

The compositions for the diagnosis, prevention and treatment of

human malignancies, for stimulating the development of cancer in a

composition is useful for inhibiting the development of cancer in a

composition is useful for stimulating the development of cancer in a

composition is useful for stimulating and/or expanding T cells specific for

Her-2/Neu polypeptide and for inhibiting the development of cancer in a

composition is useful for stimulating a T cell response in a

composition is useful for stimulating a T cell response in a

composition is useful for stimulating a T cell response in a

composition is useful for stimulating a T cell response in a

composition is useful for stimulating a T cell response in a

composition in a parophylax molecules with complementary stretches of the

continue Her-2/Neu gene fragments of interest, to isolate a full

continue and in a maprophiate host cells. The composition is useful in

prophylactic or therapeutic applications and for the treatment of cancer,

continue and the sumunotherapy of breast cancer and other Her-2/Neu-

second in a solution is useful in gene therapy. The
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                                                                                                                                                                                                                                                                                                                             Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
                                                      GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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Mcneill PD, Vedvick
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                                  MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                               ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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8; Mismatches
97.68;
 Best Local Similarity 97.61
Matches 1225; Conservative
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                                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLFSETDGYVAPLTCSPQPEYV
                          AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                         NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain.
                                                                                                                                                                                                                                                                                                                  Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185; tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                                                                          Human Her-2/neu oncogene-encoded p185 glycoprotein
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preferred fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltapD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
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97.6%; Pred. No. 0;
iive 8; Mismatches 22;
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Zhneu or a polyncleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelomenous leukaemia (AML), chronic myelomen leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-Zhneu polypeptide.
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97.6%; Pred. No. 0;
ive 8; Mismatches
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Matches 1225; Conservative
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                                                                                                                 YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNMCMQIAKGMSYLEDVR
                                                                LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRFT
                                                                                                                                                      IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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                                                   LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904
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                                                                                                                                                                NOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
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Pred. No. 0;
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(CREA-) CREATIVE BIOMOL
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HER2 transg
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HER-2/neu p
                                                                                                                        July 22, 2003, 08:41:54 ; Search time 36.7573 Seconds (without alignments) 4527.811 Million cell updat.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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	12	6619	97.4	1255	23	AAE20479		Her-2/neu	
		6619	97.4	1255	23	AAM51143		neu/	
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		6302	92.0	1200	2 5	AA036923		Human breast cance	
		5861.5	86.2	1256	23	AAB21199		Rat HER-2/new prof	
		5861.5	86.2	1256	23	AAM51144		Rat Her-2/neu onco	
tes/sec		5836.5	85.9	1256	21	AAB21206		Mouse Her-2/neu pr	
		5836.5	85.9	1256	22	AAG62860		Amino acid sequenc	
		5836.5	85.9	1256	23	AAM51151		Mouse Her-2/neu on	
		4817	70.9	919	21	AAB21203		Human HER-2/neu fu	
1249		4817	70.9	919	23	AAM51148		Her-2/neu extracel	
		4067.5	59.9	920	23	AAM51152		Mouse Her-2/neu ex	
		4067.5	59.9	926	23	AAM51153		Mouse Her-2/neu ex	
-		3701	54.5	712	21	AAB21204		Human HER-2/neu fu	
		3701	54.5	712	23	AAM51149		Her-2/neu extracel	
		3554	52.3	782	18	AAW19764		Her2-GM-CSF immuno	
		3550	52.2	653	21	AAB21200		Extracellular HER-	
		3550	52.2	653	23	AAM51145		Human Her-2/neu on	
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		100	7.0	470	15	AAKU8222		Extracellular port	
		2115	0.0	1210	1 .	AMB19239		Amino acid sequenc	
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		2112	0.0	1210	7 0	AAM30 / 68			
		2113		1210	77	AAB58420			
		3085	4.0	583	5.5	AAE20483			
		3085	45.4	587	23	AAE20481		protein	
		3083	45.4	583	23	AAE20484		protein	
		3083	4.0	009	23	AAE20482		protein fo	
		3074	45.2	1210	23	ABP51768		Human epidermal gr	
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T helper epitopes were identified (see features table). The method
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/note= "suitable for foreign epitope
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|abel= Ligand_binding_domain
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/label= Cysteine_rich_domain
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Birk P, Karlsson G;
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Herz) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APC8) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 Eirst T helper cell group which is foreign to the animal. Analogues of human PSM, human Herz and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Herz, respectively.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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97.0%; Pred. No. 0;
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Matches 1222, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MHC; immunoregulatory; immune response; HER-2; adoptive immunotherapy; anti-cancer; breast cancer antigen, APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tyrosine kinase-type receptor, HER-2
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex. (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducting an immune response in a subject and for use in adoptive immunotherapy. They are useful as compoundts of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HRR-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and 9185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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              KETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      construct encoded protein
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16-MAR-2000; 2000US-0189844
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is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endomerrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, sstrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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Best Local Similarity 97.0%; Pred. No. 0;
Matches 1222; Conservative 6; Mismatches
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                                     Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-mayransinoid conjugate; cancer; tumour; breast; ovastomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; immunological disorder; inflammatory disorder; angiogenic disorder; immunological disorder.
LEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIL
                       RRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIM
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05-OCT-2000; 2000US-238327P.
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(SCHW/) SCHWALL R.
(SLIW/) SLIWKOWSKI M.
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treatment of malignancies with which the HER-2/neu oncogene is
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/label= Intracellular domain
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Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, overian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host calls for use in immunisation. Alternatively, animal calls are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
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RRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIM
             DLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPL
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                                                                                                             DLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPL
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QPEYVNOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPCKNGVVKDVFAFGGAVENPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as pl85 or c-erbB2).
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                                                                                                                                       QPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPE
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96.9%; Pred. No. 0;
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Matches 1221; Conservative
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The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is colluture and binds to a complex of an epitope (I), bound to a chuman leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino condition and that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (III) comprising (II) and apharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (II); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimular activities, and can be used in vaccines. (I), (II) cand (III) are useful for inducing callular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for inducing callular immune response for the prevention and treatment of cancer. (I) and (III) are useful for inducing callular immune response to a tumour-associated antigen when incubated with a T lymphocyte to (I) or (II). Epitope cancines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple cumour-associated antigens from the same pathogen. Epitope-based anti-tumour sasociated and antigen selected antigens from the same pathogen. Epitope-based anti-tumour sasociated and antigen is eliminated. The vaccine cumultiple tumour-associated and and selected antigen selected antigens from the same pathogen. Epitope-based anti-tumour variability and reducing the likelihood of tumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
1136 QPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPE 1195
                                                                                                                                                                                                                                                                                                                                                                                              Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                    1196 YLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                              YLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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cellular immune responses for the prevention and treatment of cancer
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                                                           DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                            LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                                               DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVL
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tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative diseases or e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                                                   OPEYVNOPDVRPOPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPE
                                                                                  QPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPE
                                     1076 APSECAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSP
                                                                                                                                                                                                                                                                                                 Human; Her-2; epidermal growth factor receptor 2; infection; cance. hyperproliferative disorder; prophylaxis; inflammation; antisense; tumour; gene therapy; phosphorothioate backbone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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96.9%; Pred. No. 0;
iive 6; Mismatches
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Best Local Similarity 96.9
Matches 1221, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated Her-2/Neu polypeptide composition

effective for eliciting an immune response. The invention is useful for

eliciting an immune response in a patient, where the patient is human

leukcoyte antiqen (HLA)-1944 positive or is affected with breast cancer.

The composition is useful for the therapy and diagnosis of cancer.

The compositions for the diagnosis, preventions, e.g., vaccine
and other compositions for the diagnosis, prevention and treatment of
human malignancies, for stimulating and/or expanding T cells specific for
Her-2/New polypeptide and for inhibiting the development of cancer in a
containent. The invention is useful for stimulating a T cell response in a
human patient, as probe or primer for nucleic acid hybridisation, to
contained and for inhibiting the development of cancer in a
contained and for inhibiting the development of cancer in a
contained and for a thinhibiting a T cell response in a
human patient, as probe or primer for nucleic acid hybridisation, to
contained and form duples molecules with complementary stretches of the
centire Her-2/New gene or gene fragments of interest, to isolate a full
contained malignation and suitable library, and to direct expression of a
copyphylactic or therapeutic applications and for the treatment of cancer,
contained malignancies. The invention is useful in gene therapy. The
Location/Qualifiers
1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
                                                                                                                                                                                                                                                  Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                      YLTPOGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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Query Match

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                                                                                                   APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSP
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comprising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of a her-2/neu protein is fused to a Her-2/neu intracellular domain of phosphorylation domain (or its Deltapp fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ax vivo with a nucleic acid cells to the animal. The fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. The cluston protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.
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                                                                                                                                                                                                             GVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSY
                        GVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNMCMQIAKGMSY
                                                                                      LEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIL
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLI
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904.
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Disclosure; Page 71-74; 74pp; English

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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polyputleotide encoding an immunogenic Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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Perfect score:
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Maximum DB
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O9v1x8 ephydatia f			9	rattus			Q923v5 rattus nor	P11776 xiphophorus	Q8szw1 drosophila	O99162 xiphophorus	Ogovz4 xenopus lae	Ogbud7 homo sapien	Q9bq66 oryctolagus	Ognivs biomphalari	093457 scophthalm	OBuw85 paralichthy			Q9u5a8 bombyx mori	Q8uw84 paralichthy				O9dvw4 rattus sp.		Q07912 homo sapien	Ogumq4 homo sapien	O92809 abelson mur
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1193	1368	1717	527	478	599	165	176	346	435	311	1362	331	149	1671	1418	1368	1369	1358	1472	1412	1418	1245	2144	1371	1055	1036	1091	981
18.4	17.3	16.9	16.6	14.7	13.9	13.3	13.1	11.9	11.4	11.1	11.0	10.8	10.6	10.5	10.1	10.0	9.7	9.7	9.5	9.5	9.3	9.1	9.1	9.1	9.8	9.6	8.5	8.3
1250	1176.5	1148	1126	1001.5	942.5	906	887	806.5	778	754.5	744.5	734	723	713	989	682.5	661.5	959	648.5	643	633.5	619	617.5	617	586.5	586	574.5	565.5
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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CAMINALIS EAMILIARIS (DOG).

CAMINALIS EAMILIARIS (DOG).

RA YOKOLA H.;

RA YOKOLA
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Earp H.S.; "A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively epliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                         VENPEYLTPQCGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSP
                                              QPEYVNQPDVRPQPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGGA
                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000419; Euk_pkinase.
R InterPro; IPR000174; Furin-like.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Ffam; PF00057; Purin-like; 1.
R Pfam; PR001030; Recep_L L
R Pfam; PR001030; Recep_L L
R Pronom; PR00109; TyrKKINASE.
R ProDom; PR00109; TyrKKINASE.
R PROSTIE; PS00107; PR0TEIN KINASE_DOM; 1.
R PROSTIE; PS00109; PROTEIN KINASE_DOM; 1.
R PROSTIE; PS00109; PROTEIN KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1209;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINEISHER, TISSUE-LIVER;
MEDLINE-90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
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                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 3109; DB 11;
Pred. No. 8.7e-226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
Guttridge K., Dawson T.L., Earp H.S.;
Submitted (1999) to the EMBL/GenBank/DDBJ
EMBL; M37394; AAR14008.1;
HSSP; P11362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petch L.A.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                       PRT; 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
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LDVPV 1259
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                                                           MELAAWCRWGLLLALLPSGAAGTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
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| SAVVGILLAVVVGLVLGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIL
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                                           MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                          Gaps
                       22;
  Length 1259;
                       Indels
                       69
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9
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 90.1%; Score 6124; DE 89.5%; Pred. No. 0; ive 42; Mismatches
              Best Local Similarity 89.5
Matches 1132; Conservative
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EYLNTAQ------PTCLSSGFDSSALWIQKGSHOMSLDNPDYQQDFFPKEAKPNGIF 1186
                                                                      PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET---DGYVAPLTCS
                            SSLSANSN----SSTVACINRNGSCRVKEDAFLQRYSSDPTSVLTEDNIDDTFL-----
                                                         PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP
                                                                                                      EYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
STRAIN=C57BL/6J;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C3H/J01, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                         09EP99;
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor isoform 1.
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MGD; MGI:95294; Egfr.

InterPro: 1FR000345; CytC heme bind.
InterPro: 1FR000345; CytC heme bind.
InterPro: 1FR00019; Euk_pkinase.
InterPro: 1FR002104; Furin-11ke.
InterPro: 1FR002104; Furin-11ke.
InterPro: 1FR001290; Ser thr pkinase.
Ffam; PF00069; Pkinase; 1.
Ffam; PF00069; Pkinase; 1.
Ffam; PF01030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SWART; SM00261; FU; 5.
SWART; SM00220; STRC; 1.
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                                                                                                                                                   KGTPTAENPEYLGLDVP 1248
                                                                                                                                                                                                                                PRELIMINARY;
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                                     LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                           TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ
                                                                                                                                                                                                       CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
                                                                                                                                                                                                                    CAAGCTGPRESDCLVCHRFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKC
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  Gaps
639; Conservative 161; Mismatches 357; Indels 120;
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SDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCWMID 956
                             SECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAE
                                          EYLVPQQGFFCPDPAPGAGGWVHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEGA
                                                                                                       EYLTPQQGFF-----SRTPLLSSLSA
                                                                                                                                   GSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET - - DGYVAPLTCSPQPEY
                                                                                                                                                     VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-T
                                                                                                                                                                                                                  VNQ-SVPKRPAGSVQNPVYHNQPLHP-----APGRDLHYQN--PHSNAVGNPEYLNT
                                                                                                                                                                                                                                              POGGAAPOPHPPPAFSPAFDNLYYWDQ-----DP-----PERGAPPSTFKGTPT
                                                                                                                                                                                                                                                                      1142 AQ-----PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGIFKG-PT
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STRAIN=RIO PURIFICATION;
MEDLINE=89241172;
Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., D
Altschmied J., Schartl M.;
"Activation of the Xmrk proto-oncogene of Xiphophorus
overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor tyrosine kinase proto-oncogene.
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                                                                                                                                                                        LLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRN 73
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                                                                                                                                                11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
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                                                                                                                        Gaps
                                                                                                                       Indels 116;
                                                                                             Length 1210;
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Receptor; Transferase.
SEQUENCE 1210 AA; 134840 WW; 62CD021C9DE32E18 CRC64;
                                                                                        Query Match
Best Local Similarity 49.5%; Pred. No. 1.4e-223;
Matches 630; Conservative 163; Mismatches 363;
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                                                                                                                                                                                                          -----EYVNOPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTN 1106
                  VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE 1004
                                                                      DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA 1064
                                                                                                                                                                                                                                                                  1107 ONSL---PLVSSGSMDDPDY---OAG------YQAAF-----LPQTGALTGN 1141
                                                                                                                                              1019 --EPCIPPNGH--------PVRENSIALRYISDPTQNALEKDLDGH--
                                 939 VYMIILKCWMIDPSSRPRFRELVGEFSQWARDPSRYLVIOG---NLPSPSDRRLFSRLLS
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=HINDBRAIN,
MEDLINE=99263203; PubMed=10328884;
MEDLINE=99263203; PubMed=10328884;
MEDLINE=99263203; PubMed=10328884;
MEDLINE=99263203; PubMed=10328884;

"Distribution of neuregulin-1 (nrgl) and erbB4 transcripts
embryonic chick hindbrain.";
embryonic chick hindbrain.";
EMBL, AR121963; AR331764.1;
HSSP; Pl1362; IFGK.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
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PROSITE; PS000109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN_1.
KINASE; TYCOSING-PROTEIN KINASE.
SEQUENCE 1137 AA; 127927 WW; 4D616436
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InterPro; IPR000194; Euk_pkInase.
InterPro; IPR001194; Furin-like.
InterPro; IPR001368; TVFR c6.
InterPro; IPR001369; TVFR c6.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; XIP_motif.
Pfam; PF00059; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recept L domain; 1.
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ProDom; PD000001; Euk_pkinase; 1.
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996 SDD--DVVDADEYLL-----
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1142 GMFLPAAENLEYLGL 1156
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SMART; SM00219; TYTKC; 1.
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                                                                                                                                                      VQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA
                                                                                                                                                                                                          176 NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTD
                                                                                                                                                                                                                                                                                                                         HNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
                                                                                                                                                                                                                                                                                                                                                           CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 YKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAE----
                                                                                                                                                                                                                                                                                                                                                                                                                    CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGM----QYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 KANSKFIGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521 SCLHVDRGGRCVASCNLLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGFGPANCSKCAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - ORASPLTSIQYIKANSKFIGITELKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA
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                                                                                                             Gaps
                                                                                  Length 1165;
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SEQUENCE 1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                                                                                            Indels
                                                                               39.6%; Score 2693; DB 13;
llarity 45.6%; Pred. No. 2.2e-194;
Conservative 156; Mismatches 386;
                                                                             Query Match
Best Local Similarity
Matches 581; Conserv
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Length 1137;

Best	Pred. No.	DD 1011 DLQAVDNPEYHNAPNGQPKAEDEYVN
Match	Matches 533; Conservative 165; Mismatches 358; Indels 83; Gaps 26;	OV 1201 PHPPPAFSPAFDNLYYWDODPPERGA PPST
රු සි	161 LCYQDTILWKDIPHKNNQLALTLIDTNRSRACHPCSPWCKGSRCWGESSEDCOSLTRTVC 220	1056
ò	221 AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF 279	RESULT 6
qq	62 AEQCDGRCYGPYVSDCCHRECAGGCSGPKDTDCFACHNFNDSGACVTQCPQTFVYNPTTF 121	F79754 PRELIMINARY; PRT; 1328
۵ ۵	ESMPNPEGRYTPGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCA	1997 (TrEMBLrel. 03, 1997 (TrEMBLrel. 03, 1997)
8 8	122 UBBHNHNANIIIOAFCVANCEHNIV-VDSSSCVKACESSNABV-EENGINACHECIDICF 179 340 RVCYGLGMOYTKANSKFIGITELE-FAGCKKIFGSLAFLPESFDGDDASNTAPLOPEOLO 398	ErbB3. Fuch rubring
3 43		Eukaryota, Metazoa, Chordata, Crania Actinopterygii, Neopterygii, Teleost
ò	399 VPETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSL 458 	OC Acanthomorpha; Acanthopterygii; Percomor; OC Tetraodontidae; Takifugu. OX NCBI TaxiD=31033;
q	239 IFQTVREITGYLNIQSWPENMTDFRVFSNLVTIGGRALYSGLSLLILKQQGITSLQFQSL 298	
ò		
a	299 KQISAGNIYITDNSNLCYYHTVNWTSLFSTPSQKTVIHRNKKAENCTADGMVCNELCSSD 358	RT "Analysis of 148 kb of genomic DNA around RT rubripes.";
ò	HCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCQP-QNGSVTCF	-
q	359 GCWGPGPDQCLSCKRFIRGRTCIESCNLYDGEFREFANGSVCMECDPQCEKMEDNMITCY 418	
ò	578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637	InterPro; IPR000719; Euk pki InterPro: IPR002174: Furin-1
QQ	419 GPGPDHCTKCFHFKDGPNCVEKCPDGLQGANSFİFKYADEDRECHPCHPNCTQGCRGP 476	
ò	638 DDKGCPAEQRASPLTSIQYIKANSKFIGITELKRRQQKIRKYT 680	Pfam, PF00069; pkinase; 1. Pfam: PF01030: Recep L domain:
Op	477 ASHDĆIYYPWTRQSTLPQHAR-TPLIAAGVIGGLFIIVIMGLTFAVYVRRKSIKKKRA 533	
ò	681 MRRLLQETELVEPLTPSGAMPNOAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENV 740	DR SMART; SM00219; Tyrkc; 1. DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
ପ୍	534 LRRFL-ETELVEPLTPSGTAPNQAQLRILKETELKRVKVLGSGAFGTVYKGIWVPEGETV 592	PROSITE; PSS0011; PROTEIN_KINASE_DOM; ATP-binding: Transferase.
ò	741 KIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLIGICLTSTVQLVTQLMPYGCL 800	
qq	NETTGPKANVEFMDEALIMASMDHPHLVRLLGVCLSPTIQLVT	Query Match 33.2%; Score 2259;
ò	801 LDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGL 860	nocal Similarity 10:11, from
q	653 LDYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGL 712	Oy 9 WCLLLALLPPGAASTQVCTGTDMKLRI
ò	ARLLDIDETEYHADGGKVP	Db 4 WRLILMCVASRLRAASSQTQEAVCPGTQNGLSC
a	113 ARLLEGDEKEYNADGGKMPIKWMALECIHYRKFTHQSDVWSYGVTIWELMTFGGKPYDGI 772	Qy 63 TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVI
ò	921 PAREIPDLEKGERLPOPPICTIDVYMIMVKGWMIDSECRPRERELVSEFSRMARDPORF 980	Db 64 TQIESNWDFSFLKTIREVTCYVLIAMNHFQEII
QQ	SRPKFKELP	Qy 123 LNNTTPVTGASPGGLRELQLRSLTEILKGGVL
ò	981 VVIQNED-LGPASPLDSTFYRSLLEDDDMGDLVDAESYLVPQQGFFCPDPAPGAGGMVHH 1039	Db 121YPKDGPSGLNQLGLMNLTBILDGGVQ
QQ	ω.	Oy 183 LIDTNRSRACHPCSPMCKGSRCWGESSEDCOSI
λ	1040 RHRSSSTRSGGGDLTLGLEPSEEAPRSPLAP-SEGAGSDVFDGDLGMGAAKGLQSLP 1096	Db 174 IQFNGERGVCHKSC-GNYCWGPGKDQCQII
q	892 NRNGFVYRDGGYAAEGGV-PMPYRAPGCIIPEAPVAQGATAEIFEDTCCNGTLRKQVATL 950	Qy 242 AGCTGPKHSDCLACLHFNHSGICELHCPALVTY
ò	1097 THDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG 1149	Db 230 AGCKGPLDTDCFACRLFNDSGACVPQCPQTLIT
q	. 951 AKEDSSTQRYSADPTVFIPERVIRGELDEDGYMTPMRDKPKTDYLNPVEENPFVSRRKNG 1010	Qy 302 NYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEI
δ	1150 PLPAA-RPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQ 1200	-VDGSSCVSVCPPDKMEVERC

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VNEPLYLNTFANTLENAEYL-----K 1055
               TLIQRNPQLCYQDTILWKDIFHKNNQLALT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYNTDIFESMPNPEGRYTFGASCVTACPY 301
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..7e-161;
les 417; Indels 196; Gaps
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Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
pha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                   -FAVSQGGHIGYLPMSPSPVDTIRQLWYQRSRLSSVRTLPDRSAFRRSSREAELCEDGAQ 1103
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                              479
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                                                            VPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                                     SCPAGVN-DGEKGLIFKFPNREGHCEPCHQNCTQGCSGPGLNDCLEAARLIISSGQITG
                                                                                                                                                      IQY-IKAN-----SKFIGITELKRRQQKI-RKYTMRRLLQETELVEPLTPSGAMPNQAQ
                                                                                                                                                                YVAAGVGSPYVSRLLGICLTSTVQLVTOLMPYGCLLDHVRENRGRLGSQDLLANMCMQIAK
                                                                                                                                                                                                                           ELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL
        ECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
                                                                                                                        ARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQR----ASPLTS
                                                                                                                                                                                    706 MRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEA
                                                                                                                                                                                                                                                                                                                                            .006 DDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAP
                                                                                                                                                                                             699 ARILKPSDLRKIKPLGSGVFGTVSKGFWIPEGETVKIPVAIKTIQDSSGRQTFTEITDHL
                                                                                                                                                                                                                                                                                                                              Q3-----
                              PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
                                                                                                                                                                                                                                                                                                                                                                           1066 RSPLAPSEGAGSDVFDGDLGMG---AAKGLOSLPTHDPSPLQ------RYSEDPTV
                                                                                                                                                                                                                                                                                                                                                                                           -----GLGDRFATPSLQPSPSWSTSPSQINSYMVMTQLRYD----
                                                                                                                                                                                                                                                                                                                                                                                                         1113 PLPSETDGYVAPLTCSPQP-EYVNQ-------PDVRPQPPSPREGPL--PAAR
                                                                                                                                                                                                                                                                                                                       939 YMVMVKCWMIDENIRPTFKELASDFTRMARDPPRYLVIRMEG------
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09BIH9, PRELIMINARY; PRT; 1433 AA. 09BIH9; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Putative epidermal growth factor receptor (Fragment)

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86 IAHNOVROVPLORLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGLREL 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PESFDGDPASNT-----APLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRN
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1433;
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159585 MW; E3D9D88967724F07 CRC64;
                                                                                                                                                                              "Cloning, expression and localisation of the Anopheles epidermal growth factor receptor"; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ301655; CACJ5008.1; HSSP: P11362; IFGK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2e-141;
                                                                                                                                                                                                                                                                                 InterPro; IFR000145; CytC heme bind.
InterPro; IFR000149; EGFR L domain.
InterPro; IFR000149; EGFR L domain.
InterPro; IFR001749; Euk phrase.
InterPro; IFR001249; Ser thr pkinase.
InterPro; IFR001249; Ser thr pkinase.
InterPro; IFR001245; Tyr pkinase.
InterPro; IFR001245; Tyr pkinase.
InterPro; IFR00146; Tyr pkinase.
InterPro; IFR00146; Tyr pkinase.
InterPro; IFR00146; Tyr pkinase.
InterPro; IFR00140; Recept L domain; 2.
InterPro; IFR00140; Recept L domain; 2.
InterPro; IFR00140; TyrkINASE.
INTS; SM002215; ITR; 7.
INTS; SM002215; Trk; 1.
INTS; PR00119; PROTEIN KINASE DOM; ITPROSITE; PS00110; PROTEIN KINASE DOM; 1.
INTS; PROSITE; PS00110; PROTEIN KINASE DOM; 1.
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29.3%; Score 1993.5;
Best Local Similarity 32.2%; Pred. No. 2.2e-
Matches 466; Conservative 194; Mismatches
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1433 AA;
                                                                                                                        SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=7165;
                                                                                                                                                                 Lycett G.J.;
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NON TER
SEQUENCE
                                                                Anopheles.
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                      Homo sapiens (Human)
                                                                                                            SEQUENCE FROM N.A.
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                                                                                     NCBI_TaxID=9606;
                                Herstatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                   |:::|:|:| | :|||| ||:||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| AKDVPELIEIGHKLPQPDICSLDVYCILLSCWVLDADARPTFKQLAETFAEKARDPGRYL 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGG 1183
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                                                                                       618
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 PHOALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTOCVNCSQFLRGQECVEECRVLQ 548
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                                                                                                     562 NGTCINCHKTCVGCRGPRDTIAPDGCISCDKAIIGSDAKIERCLMKDESCPDGYYSDYVL 621
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                                                                                                                                                                                                                                                                                  TWALAGCEDSEPLRPSNVGPNLTKLRIIKEAEIRRGGVLGMGAFGRVFKGVWMPEGESVK 861
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                                                                                                                                                      QEEGPLKQLSGKAVCRKCHPRCKKCTGYGFHEQFCQECTGYKKGEQCEDECPQDFYANEE 681
                                                       982 VIQNEDLGPASPLDSTFYRSLLEDDDMGDLV-------
           SDHEVWVQKNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLDSCK---
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                                                                                       ----SGVKPDLSYMPIWKFPD-----
                                                                                                                                                                             --ACOPCPINCT-----HSCVDL-----DD-----KGCPAEQ-----
                                           GLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                  MEDLINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secreted autoinhibitor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                              Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., He Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AR177761, AAD56009.2; ... InterPro; IPR00494; EGFR L. domain. InterPro; IPR002174; Furin-Tike. Pfam; PF00157; Furin-like; 1. Pfam; PF00157; Furin-like; 1. SWART; SMORGI; FU; Admain; 1. SWART; SMORGI; FU; A 5472 MM; FECIBE347E2D030C CRC64;
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Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 1871; DB 4;
98.8%; Pred. No. 6.2e-133;
iive 1; Mismatches 3;
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Strausberg R.;
Submitted (APR-2002)
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EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV 1122
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                                                                                                                    943 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL 1002
                                                                                                                                                                                               1003 LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE 1062
                                                                                                                                        61 IDVYMIMVKCHMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL 120
                                           983 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GAVENPEYLTPQGGAALSPTLLLPSAQPSTTSITGTRTHQSGGLHPAPSKGHLRQRTQST 360
                                                               1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT 60
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MEDLINE=94203659; PubMed=8152791;
Wennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Beug H.; CerbB proto-oncogene sequences: rapid "Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes with different transforming capacities.";
Oncogene 9:1307-1320(1994).

EMBL; S69372; AAGG0725.1; -.

HSSP; P03322: 1A6S.
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ive 69; Mismatches 125; Indels 106;
     53;
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InterPro; IPR001019; Euk pkinase.
InterPro; IPR001019; Tyr_pkinase.
Ffam; PP00669; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
ProDom; PR00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914FFEID63 CRC64;
     22; Indels
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
NCBI_TaxID=11950;
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     Mismatches
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     330; Conservative
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POLYPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEY 1242
                                                                                                                                                          942
                                                                                                                                                                                                                                                   61 IDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPSSPMDSTFYRSL 120
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                                                                                                                                                                                                                               943 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
Wan D.F., Gu J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1697.5; DB 4; Length 412; Pred. No. 7.8e-120;
                                                                                 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wan D.F., Gu J.R.;
"Novel human cDNA clones with function of inhibiting cancer
                                                                               Length
                                                                                                                  Indele
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                       40163 MW; OBE03395F9E101B0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 44.7 kDa protein.
                                                                             $; Score 1739; DB 11;
8; Pred. No. 4.8e-123;
11; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AA
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SMART; SM00219; TyrKC; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR002048; EF-hand.
InterPro; IPR00119; ENC pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00069; pkinase; I.
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80.5%;
                                                                             Query Match 25.6%;
Best Local Similarity 88.0%;
Matches 323; Conservative 1
EMBL; BC027080; AAH27080.1;
Hypothetical protein.
SEQUENCE 367 AA; 40163 MK
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991 ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGG 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 GERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKMARDPPRYLVIQGDERWHL 414
                                                                                                                                                                                                                               578 GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 HAEGGKVPIKMMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGP 990
                                                                                                                                                                                                                                                                                                                                                     175 ATSPKANKEILDEAYVMASVDNPRVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNI 234
                                                                                                                                                                                                                                                            GP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                              415 PSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF-----NSPST----
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MEDLINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
"Six amino acids from the retroviral gene gag greatly enhance the transforming potential of the oncogene v-erb-B.";
                                                                                                                                                                                    Indels 106;
                                                                                                                                         Length 567;
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                                                                                             CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
03-V-ERD-A, V-ERB-B protein.
GAG, V-ERB-A, V-ERB-B.
Avian erythroblastosis virus.
                                                                                                                                    24.6%; Score 1675; DB 15; 54.6%; Pred. No. 6.3e-118; ive 67; Mismatches 119;
                                                                                             C6D9CBA7ADF725E1
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PROSITE; PS50011; PROTEIN KINASE DOM; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1. Tyrosine-protein kinase.
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                                                                                             63390 MW;
                                                                                                                                                                 Best Local Similarity 54.6
Matches 351; Conservative
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       PEETATPKTGP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHP 197
                                                                                                                                                                                                                                    PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLD
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                                                                                           198 NCTRGCKGPGLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRRHIVRKRTLR
                                                                                                                                                                 RLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKI
                                                  NCTHSCVDLDDKGCPAEQRASPLTSIQYIKANSKF-----IGITELKRRQQKIRKYTMR
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Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes w: different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL; S69372; AAC60727.1; -.
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Viruses, Retroid viruses, Retroviridae, Alpharetrovirus.
VCBI_TaxID=11950;
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InterPro; IPR001745; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
SMART; SM00219; TYRKC; I.
PRODm; PR000019; TYRKC; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP; I.
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                                                                                      1161 LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.7%; Score 1610.5; DB 15; Length 962; Best Local Similarity 50.9%; Pred. No. 1e-112; Matches 352; Conservative 67; Mismatches 149; Indels 123; Gaps
Chocogene 5:15-24(1990).

C. '- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C. '- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

EMBL; X52209; CAA36459.1; -.

BMBL; X52211; CAA36459.1; -.

BMBL; SMO0104; -.

BMART; SMO0104; -.

BMART; SMO0104; -.

BMART; SMO0109; -.

BMART; SMO0199; -.

BMART; -.

BMART
                                                                                                                                                                                                                                                                                                                                                                                                                               962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
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REQUENCE FROM N.A.

RECURINE-88217326; PubMed=2897102;

RECURINE-88217326; PubMed=2897102;

RECURING-88217326; PubMed=2897102;

RECURING-88217326; PubMed=2897102;

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT "Common site of mutation in the erbB gene of avian erythroblastosis

RT Virus mutants that are temperature sensitive for transformation.";

REMBL, X06943; CAA-0024-1; -

REMBL, X06943; CAA-0024-1; -

RICEPTO, IPRO01245; Tyr_pkinase.

REMBL, X069019; PKINASE TYP; 1.

REMBL, REMONITE; PROOTEIN KINASE ATP; 1.

REMOSITE; PS500117; PROTEIN KINASE TYP; 1.

REMOSITE; PS500107; ROTEIN KINASE TYP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (T834) v-erbB gene.
Avian erythroblastosis virus.
Viruses, Retroid viruses; Retroviridae; Avian type C retroviruses.
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543
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KX MEDLINE=21085660; PubMed=1127851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAAKawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azakwa T., Yara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustiniche S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

A Lyons P., Marchionni L., Maabima J., Mazzarelli J., Mombaerts P.,

Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nacione P., Ring B., Ringwald M., Redriguez I., Sakamoto N.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hayashizaki Y.,

Hayashizaki Y.,
ASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGG 1050
                                                                                                                  1051 GDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQR 1105
                                                                                                                                                                                                                           1106 YSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LERA 1164
                                                                                                                                                                                                                                                                                     ------PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQIQIYNYISLTAISKL 524
                                                         ----NSPST----
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"Alternative Transcripts from the Human and Mouse EGFR Genes Encode
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELUSIONE FROM N.A.
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A. Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threaddill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
Maihle N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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300 VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRKVCNGIGIGEFK-DTLSINAINIK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 -FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLBEITGYLYISAWPDSLPDL
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Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%; Score 1506.5; DB 11; Lengt 44.5%; Pred. No. 4.2e-105; ive 97; Mismatches 233; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72906 MW; 6B34063B1BC928CB CRC64;
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                                                                                                             EMBL; AF124513; AAD44149.1; EMBL; AF275366; AAG28047.1; EMBL; AF275364; AAG28047.1; JOINED. EMBL; AF076494; BAB2368.1; EMBL; AK004944; BAB23641.1; EMBL; AK004911; BAB23641.1; EMBL; AK004911; EMBL; AK04911; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
SMART; SM00261; FU; 3.
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Search completed: July 22, 2003, 09:24:14 Job time : 51.6008 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                           OM protein - protein search, using sw model
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July 22, 2003, 08:47:04; Search time 10.5911 Seconds (without alignments) 4891.279 Million cell updates/sec Run on:

SEQ4-632-652-12 6796 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1249 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_40:*

Database :

SUMMARIES

Result	9700	Query Match	Length	DB	OI	Description
		4 60		-	ERB2 HUMAN	1 9
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EPB1 CHICK RET HUMAN	EPBI RAT FAKI XENLA	EPB4 HUMAN	FAKI MOUSE FAKI RAT	ABL MLVAB	FAKI HUMAN EPA2_MOUSE
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ALIGNMENTS

N. S. C.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 6619; DB 1; Length 1255;
Pred. No. 0;
6; Mismatches 17; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR 004078.
1170 1170 P -> A (IN REF. 2).
1255 AA; 137909 MW; 39E9DFDA04DCF962 CRC64;
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FTId=VAR
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Best Local Similarity 96.9%;
Matches 1221; Conservative
      576
584
584
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634
1139
1248
124
187
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensea greement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782, ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.202. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOW; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

ATP (BY SIMILARITY).

BY SIMILARITY.

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InterPro; IPR000494; EGFR L domain.
InterPro; IPR00219; Euk Dkinase.
InterPro; IPR002145; Purin-like.
InterPro; IPR004019; YLP_motif.
Ffam; PF00757; Purin-like; 1.
Pfam; PF01030; Recep L domain; 2.
ProDom; PP000001; Euk Dkinase; 1.
SWART; SW00261; FU; 3.
                                                                                                                                                                                                                                                                                                                                        EMBL; M11767; AAA35808.1; ---
EMBL; M11761; AAA35808.1; JOINED.
EMBL; M11762; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11763; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M11765; AAA35808.1; JOINED.
EMBL; M12765; AAA35808.1; JOINED.
EMBL; M12765; AAA35808.1; JOINED.
EMBL; M2043, AAA35493.1; --
FIRI, A25491; A25491.
FIR; A25491; A25491.
FIR; A24571; A24571.
FIRS, P11362; IFGK.
GGREW; HGNC: 3430; ERBB2.
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SIGNAL
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KETELRKVKVLGSGAFGTVYKG1WIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMA
             KETELRKVKVLGSGAFGTVYKGIMI PIGENVKI PVAI KVLRENTSPKANKEI LDEAYVMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bargmann C.I., Hung M.-C., Weinberg R.A.; "The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 37, Last amonotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p188srbB2) (NEU proteo-oncogene) (C-erbB-2) (Epidermal growth factor ERBB2 OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially
expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
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MEDLINE=92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1257 AA
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MEDLINE=86118662; PubMed=3945311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 319:226-230(1986)
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STRUCTURE
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oncogenic and oncogenic forms of the neu protein."; EMBO 11:43-48(1992).
                                                ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprofin; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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                                                                                                                                                                              RESIDUES (BY SIMILARITY).
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PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001245; Tyr pkinase. InterPro; IPR004019; YLP motif. Pfam; PF00069; pkinase; 1. Pfam; PF00757; Furin-like; 1. Pfam; PF01030; Recep L domain; 2. Pfam; PF01030; Recep L domain; 2. Probom; PD000001; Euk_pkinase; 1. SMART; SM00261; FU; 3.
                                                                                                                                                                                                                                                                                                                         EMBL; X03362; CAA27059.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                  HSSP, P11362, 1FGK.
Incerpro, IPR000494, EGFR L domain.
Incerpro, IPR000119; Euk pkinase.
Interpro, IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disease mutation.
                                                                                                                                                                                                                                                                                                                                        PIR; A24562; TVRTNU.
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SIGNAL 1
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                                                                                           1LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM
                                                                                                                                                                                                                                                                                                                                              MGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                        PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94133007; PubMed=7908275;
Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,
Yamazaki Y., Ishikawa T.;
Yamazaki Y., Ishikawa T.;
"Cloning and activation of the Syrian hamster neu proto-oncogene.";
Gene 140:251-255(1994).
-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
POTENTIAL LIGAND FOR FHIS SECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALPHA AND AMPHIREGULIN (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
8-Ceptor protein-tyrosine kinase erbB-2 precursor
(p185erbB2) (NEU proto-oncogene) (C-erbB-2).
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SUBUNIT: HETERODIMER WITH EACH OF
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6129264583011402 CRC64;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                 R InterPro; IPR000494; EGFR L domain.
R InterPro; IPR000419; Euk pkinase.
R InterPro; IPR0002174; Furin-like.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR001245; Tyr pkinase.
R InterPro; IPR004019; YLP motif.
R InterPro; IPR004019; YLP motif.
R Pfam; PF00050; Pkinase.
R Pfam; PF00075; Furin-like; I.
R Pfam; PF00100; Rub; Z.
R Prodom; PD000001; Euk pkinase; I.
R RMART; SM00261; FU; 3.
R RMART; SM00219; Tyrkci.
R RMART; SM00109; PROTEIN KINASE ATP; I.
R PROSITE; PS00110; PROTEIN KINASE DOM; I.
M Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
M Transferase; Tyrosine-protein; Multigene family; Proto-oncogene; Disease mutation;
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1070 APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSP 1129
            Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W., Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.; "Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells.",
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MEDLINE=21100872; PubMed=11161793;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D., Maihle N.J.;
                                                                                                                                                                     EGER HUMAN STANDARD; PRT; 1210 AA.
P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732;
000688; Q9B222; Q9H2C9; Q9H3C9;
01-31-JUL-1986 (Rel. 10, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor EGER OR ERBB1.
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                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Expression of a truncated epidermal growth factor receptor-like
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epidermal growth factor receptor expression in human placenta.";
Mol. Reprod. Dev. 41:149-156(1995).
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MEDLINE=95382957; PubMed=7654368;
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MEDLINE=84219729; PubMed=6328312;
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TISSUE=Placenta;
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SEQUENCE OF 1-29 FROM N.A.
MEDLINE=85270438; PubMed=2991899;
18hil S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
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"ATP-stimulated interaction between epidermal growth factor receptor
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Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
"Expression cloning of human EGF receptor complementary DNA: gene amplification and three related messenger RNA products in A431
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Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
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MEDLINE-85046483; PubMed=6093780;
Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
O'Malley B.W.;
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MEDLINE=89278137; PubMed=2543678;
Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,
Howk R., Givol D., Ullrich A., Schlessinger J.;
"All autophosphorylation sites of epidermal growth factor (EGF)
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MEDLINE=88217333; PubMed=3329716;
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BEDIANE=64245835; PubMed=63305633;
Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K.,
Roe B.A., Merlino G.T., Pastan I.;
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Nature 309:806-810(1984)
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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MEDLINE=84191554; PubMed=6325948;
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Nature 309:270-273(1984).
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                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=89225196; PubMed=8556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
"Disulfide bond structure of human epidermal growth factor receptor.";
J. Biol. Chem. 273:11150-11157(1998).
                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                 ASN-528.
MEDLINE=96398132; PubMed=8962717;
Smith K.D., Davies M.J., Balley D., Renouf D.V., Hounsell E.F.;
"Analysis of the glycosylation patterns of the extracellular domain
the epidermal growth factor receptor expressed in Chinese hamster
                                                                                                                                                                                                                                        atypical
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truncated isoform/TEGFR, 3/p110 and 4; are produced by
alternative splicing.
TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                          Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.; "Characterization of the N-oligosaccharides attached to the aty, Asn-X-Cys sequence of recombinant human epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                        CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444
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    carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                     other polypeptide
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Best Local Similarity 49.5%; Pred. No. 8.6e-157;
Matches 624; Conservative 173; Mismatches 360;
  in their carbox
EGF receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Receptors for epidermal growth factor and
receptor and HER2/neu are located in t
Identification of a novel site in EGF
J. Biol. Chem. 264:10667-10671(1989).
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                                                                                                                                                                                              ASN-603.
MEDLINE=20198209; PubMed=10731668;
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EMBL; U495089; AAB53063.1; --
EMBL; U48723; AAC50802.1; --
EMBL; U48723; AAC50804.1; --
EMBL; U48725; AAC50796.1; --
EMBL; U48725; AAC50796.1; --
EMBL; U48726; AAC50798.1; --
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LLLALLPPGAA - - STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                      LLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRN
                                                                                     ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
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           1140 RPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TPQGGAA 1198
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                                                    1199 POPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPSTFKGTPTAENPEY
                                                                                              ----PICVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGS-TAENAEY
                                                                                                                                                                                                                                                                                                                                                                                                                           Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor gene is regulated in mouse blastocystes during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J., Givol D., Morse B.; guide to study the ligand
                                                                                                                                                                                                                                                                                                                                             Avivi A., Skorecki K., Yayon A., Givol D.; "Promoter region of the murine fibroblast growth factor receptor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=B6/C3; TISSUE=Liver;
MEDLINE=94170986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S., Jenkins N.A., Lee D.C.;
"The mouse waved-2 phenotype results from a point mutation in the inceptor tyrosine kinase.";
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hibbs M.L.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eisinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93126380; PubMed=7678348;
                                                                                                                                                                                          PRT; 1210 AA.
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                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
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MEDLINE=91232866; PubMed=2030916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes Dev. 8:399-413(1994).
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Oncogene 7:1957-1962(1992)
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                                                                                                                                                                                          STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF, AND ALGO OF TGF-ALLHA, AMPHIREGULIN, HEPRAIN-BINDING EGF, GP30 AND VACCINIA VIRUS GROWTH FACTOR (8Y SIMILARITY).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                            R InterPro; IRR001245; Tyr_pkinase.

R Pfam; PF00069; pkinase; I.

R Pfam; PF00130; Recep_L_domain; 2.

R ProDom; PD000001; Euk_pkinase; 1.

R SMART; SM00261; FU; 3.

R SMART; SM00219; Tyrkc; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R Transmembrane; Glycoprotein; Receptor; Signal; Transferase;

R TYCOSINE; PS00109; POTENTIAL.

POTENTIAL.
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EPIDERMAL GROWTH FACTOR RECEPTOR
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X78987, CAA55587.1, -.
EMBL, U03425, AAA17899.1, -.
EMBL, X59689, CAA42219.1, -.
EMBL, L06864, AAA53029.1, -.
EMBL, Z12608, CAA78249.1, -.
HSSP, P11362, 1FGK.
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SECRPRFRELVSEFSRWARDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAE 1015
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 SDVWSYGVTVWELMTFGSKRYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCWMID 956
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                                                     VKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYV
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15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
(P180erbB4) (Tyrosine kinase-type cell surface receptor HER4).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
NCBI_TaxID=9606;
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TISSUE=Breast carcinoma;
MEDLINE=91189574; PubMed=8383126;
Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M.,
Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HER4/p180erb84, a fourth mepidermal growth factor receptor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993)
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Elenius K., Corfas G., Paul S., Choi C.J., Rio
Klagsbrun M.;
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1017 EYLIPOOGFF-----
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MW; 690E20D46DF2D2F5 CRC64;
BY SIMILARITY.

PROSPHORYLATION (BY PKC)
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llarity 49.5%; Pred. No. 3.3e-155;
Conservative 164; Mismatches 362;
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C-> W (IN REF. 2).
C-> W (IN REF. 5).
HP-> DR (IN REF. 4).
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DISHLFID
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C. -!- SUBGELLULAR LOCATION: Type I membrane protein.

C. -!- ALTERNATIVE PRODUCTS: 2 ISOFORNS; JM-A (SHOWN HERE) AND JM-B;

C. -!- ALTERNATIVE PRODUCTS: 2 ISOFORNS; JM-A (SHOWN HERE) AND JM-B;

C. -!- ALTERNATIVE PRODUCTS: 2 ISOFORNS; JM-A (SHOWN HERE) AND JM-B;

C. -!- ALTERNATIVE PRODUCTS: 2 ISOFORNS; JM-A (SHOWN HERE) AND JM-B;

C. -!- ALTERNATIVE SPLICING. THE TWO ISOFORNS DIFFER

C. -!- TONOLLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORNS ARE EXPRESSED IN

C. CRERBELLUM, BUT ONLY THE JM-B ISOFORN IS EXPRESSED IN THE HEART.

C. -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,

KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHROID, CERRBELLUM,

LUNG, SALIVARY GLAND, AND PANCREAS: LOWER LEVELS IN THYMUS,

LUNG, SALIVARY GLAND, AND PANCREAS.

RESIDESS.

RESIDESS.
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PUTENTIAL.

EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYSPINSAMIC (POTENTIAL).

CYSPLASMIC (POTENTIAL).

CYS-RICH.

CYS-RICH.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

                                                     5. Biol. Chem. 272:26761-26768(1997).
-!- FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND
NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF, TGF-A, AND AMPHIRECULIN.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
"A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific tissue distribution and differential processing in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; I.
Pfam; PF00069; pkinase; I.
Pfam; PF00757; Furin-like; I.
Pfam; PF00757; Furin-like; I.
Pfam; PF00757; YuPep L.
ProDom; PD000001; Euk_pkinase; I.
SWART; SM00219; Tyrk; 4.
SWART; SM00219; Tyrk; 4.
PROSITE; PS00109; PROTEIN KINASE ATP; I.
PROSITE; PS00109; PROTEIN KINASE DOM; I.
PROSITE; PS00110; PROTEIN KINASE DOM; I.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transmembrane; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                              tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000494; EGFR L domain.
InterPro; IPR000119; Euk pkinase.
InterPro; IPR002144; Purfin-like.
InterPro; IPR00145; Tyr pkinase.
InterPro; IPR004019; YLP motif.
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DOMAIN 26 1308
DOMAIN 652 675
DOMAIN 186 334
DOMAIN 196 633
DOMAIN 724 732
BINDING 751 751
ACT SITE 843 843
DISULFID 193 205
DISULFID 217 229
DISULFID 217 229
DISULFID 217 229
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BY SIMILARI BY SIM	Ve 175; Pred. No. 7.16-147; Undels 177 ve 175; Mismatches 385; Indels 177 STQVCTGTDMXLRLPASPETHLDMLRHLYQGCQVV QPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVV QPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVV QPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVV SELQLERYYLPELKGQVLINFURTGTKLYEDFHKN SELQLERSLTEILKGGVLIORNOGLCYGTLIMDIFHKN SELGLERSLTEILKGGVLIORNOGLCYGTLIMDIFHKN CELGLKRUTEILNGGVYVDQNKFLCYADTIHWQDIVRNP MCKGSRCWGESSDCQSLTRTVCAGGC-ARCKGPPPTDC H
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                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                            652 TSIQYIKANSKFI----GIT--ELKRRQQKIRKYTWRRLLQETELVEPLTPSGAMPNQAQ
                                                                                                                                                 MRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEA
TLFSTINQRIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRGRICIES
                     CRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERB4 RAT STANDARD; PRT; 1308 AA.
062956; Q9Z2N7;
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
ERBB4 OR TYRO-2.
                                                               GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
-: SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
-: SUBCELLULAR LOCATION: Type I membrane protein.
-: TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NEXVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY RECIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                                                                                                                                                                                                                                                                                                                                        Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

Expression of neuregulins and their putative receptors, ErbB2 and
ErbB3, is induced during Wallerian degeneration.";

J. Neuroed. 17:1642-1659(1997).

J. Neuroed. 17:1642-1659(1997).

J. NRG-19. HEPARILL BINDING BCF-LIKE GROWHT FACTOR, BETACELLULIN AND
NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).

CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
SIGNAL
                                                                                                                                                                                                                                                             "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                      Zhao Y.-Y., Sawyer Paliga R.R., Opel D.J., Han X., Baliga R.R., Opel D.J., Han X., Marchionni M.A., Kelly R.A.; "Neuregulins promote survival and growth of cardiac myocytes." Persistence of Erbbs and ErbB4 expression in neonatal and adult ventricular myocytes."; J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1031-1198 FROM N.A.
STRAIN=Sprague-Dawley, TISSUE=Spinal cord;
MEDLINE=97184212; PubMed=9030624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000494; EGFR L domain.
Interpro; IPR000719; Euk pkinase.
Interpro; IPR002174; Furfin-like.
Interpro; IPR001245; Tyr pkinase.
Interpro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PRO0109; TYRKINASE.
PRODOM; PROD00001; Buk pkinase; 1.
SMART; SM00261; FU; 4.
SMART; SM00219; TYRKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01030; Recep L domain; 2. Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                         FISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
                     FISSUE=Heart;
MEDLINE=98221155; PubMed=9553078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF041838; AAD08899.1; -.
EMBL; US2531; AAC53051.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                              SEQUENCE OF 848-901 FROM N.A.
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297 TACPYNYLSTDVGSCTLVCPLHNQEVTAEDCTORCEKCSKPCRARVCYGLGMOYIKANSKF 356		Db 1062 SQFVYQDGGFATQQG
-TYROSIN OTENTIAL). TY). TY). TY). (AUTO-)	CARBOHYD 579 479 N-LINEED GLUNAC (POTENTIAL). CARBOHYD 576 576 N-LINKED GLCNAC) (POTENTIAL). CARBOHYD 576 576 N-LINKED GLCNAC) (POTENTIAL). CARBOHYD 620 620 N-LINKED GLCNAC) (POTENTIAL). CONFLICT 1062 1062 S -> N (IN REF. 3). CONFLICT 1080 1082 PYT -> SYR (IN REF. 3). SEQUENCE 1308 AA, 146957 MM; D944BB0996A08B41 CRC64; SEQUENC 1308 AA, 146957 MW; D944BB0996A08B41 CRC64; Best Local Similarity 44.9%; Pred. No. 6.7e-146; Matches 605; Conservative 182; Mismatches 395; Indels 164;	

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537 GQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFC 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16891; CAA44770.2; -
DR PIR; S06142; S06142.
DR HSP; PIR36; JEFR L. domain.
HEAPPO; IPR000194; EGFR L. domain.
InterPro; IPR001244; Furin-like.
DR InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Ffam; PP00109; Furin-like; 1.
DR Ffam; PP00109; TYRKINASE.
DR PRODM; PD000001; Euk pkinase; 1.
DR FMRT; SM0020; STKC; 1.
SMART; SM00219; FYFKC; 1.
SMART; SM0019; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR TYNOSIMe—protein kinase; ATP-binding; Phosphorylation; Proto-oncogene.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
TYNOSIME—protein kinase; ATP-binding; Phosphorylation; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112).
XMRK OR TU.
                                                                                                                    Kiphophorus maculatus (Southern platyfish).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Extinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poecillidae; Xiphophorus.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MIRDLINRE-20015140, PubMed=2797166;
Witchrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,
Telling A., Robertson S.M., Schartl M.;
Novel putative receptor tyrosine kinase encoded by the melanoma-
inducing Tu locus in Xiphophorus.";
Nature 341:415-421(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELANOMA RECEPTOR PROTEIN-TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
-!- SUBCELULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PRT; 1167 AA.
STANDARD;
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665
1167
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XMRK XIPMA
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TRANSMEM
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DOMAIN
NP BIND
BINDING
ACT_SITE
                  P13388;
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195 204 BY SIMILARITY 199 212 BY SIMILARITY 199 212 BY SIMILARITY 199 220 228 BY SIMILARITY 199 224 236 BY SIMILARITY 241 253 BY SIMILARITY 256 265 BY SIMILARITY 269 296 BY SIMILARITY 269 297 BY SIMILARITY 269 297 BY SIMILARITY 269 297 BY SIMILARITY 269 253 BY SIMILARITY 269 253 BY SIMILARITY 269 253 BY SIMILARITY 260 251 BY SIMILARITY 260 261 BY SIMILARITY 260 261 BY SIMILARITY 260 261 BY SIMILARITY 260 261 BY SIMILARITY 261 261 BY SIMILARITY 261	ch 1. Similarity 45.1%; Pred. No. 1.7e-132; 571; Conservative 160; Mismatches 393; Indels 143; Gaps 29;	4 AALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 59	60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119 	20 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 :-	ALTLIDTNRS : TMNLIPHAFE	9 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDIFESMPNPEGRYTFGASCVTA 298	9 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358	9 ITEL-EFAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAMPD 4	8 SLPDLSVEQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 476 :: :	VHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLR 53	77 ANTINWERLERSEDGSIEYDARTENQTCNNECSEDGCWGPGPTM-USCLHVDR 529
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Natl. Acad. Sci. U.S.A. 86:9193-9197 (1989)

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1012 VDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAP 1071
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GGRCVASCNLLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPGPANCSKSAHFQDGPQC 589
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                                                                                                                                                                                                                                                                      597 VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAE-----QRASPL
                                                                                                                  652 TSIQYIKANSKFIGITELKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKE
                                                                                                                                      TELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 IPRCPHGILGDGDTL-IWKYADKMGQCQPCHQNCTQGCSGPGLSGCRGDIVSHSSLAVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
101-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(c-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
MEDLINE=90083234; PubMed=2687875;
Kraus M.H., Isasing W., Miki T., Popescu N.C., Aaronson S.A.;
Kraus and characterization of ERBB3, a third member of the
ERBB/epidermal growth factor receptor family: evidence for
overexpression in a subset of human mammary tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1342 AA
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ENLEYLG 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT FORM).

ALTERNATIVE RROUDCYS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
DOWAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SHY OF THE RECEPTOR MAY INTERACT WITH THE PROMINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PIPM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROWOTES ITS ASSOCIATION WITH THE PRES SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).

DISBASE: OVERREXPRESSED IN A SUBSET OF HUMAN MANMARY TUMORS.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                         Green J.M., McDonald V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                  SEQUENCE FROM N.A. MEDLINE=90311312; PubMed=2164210; Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L. Todaro G.J., Shoyab M.; Molecular cloning and expression of an additional epidermal growth factor receptor-related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R InterPro; 1PR000494; EGFR L domain.
R InterPro; 1PR000199; Euk pkinase.
R InterPro; 1PR000119; Euk pkinase.
R InterPro; 1PR000124; PurIn-like.
R InterPro; 1PR001245; Tyr_pkinase.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF001069; Pkinase; 1.
R Pfam; PF001001; Euk_pkinase; 1.
R SMART; SM00201; FU; 3.
R SMART; SM00219; TyrKc; 1.
R PROSITE; PS00100; PROTEIN KINASE ATP; FALSE NEG.
R PROSITE; PS00100; PROTEIN KINASE DOM; 1.
M Transmembrane; Glycoprotein; Multigen family; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Tyrosine-protein; Multigene family; Receptor; Signal; Alternative splicing.
SIGNAL
                                                                                                                                                                                                           TISSUE=Placenta;

BEDLINE=91202022; PubMed=7685162;

Katoh M., Yazaki Y., Sugimura T., Terada M.;

Katoh M., Yazaki Y., Sugimura T., Terada M.;

"c-erbB3 gene encodes secreted as well as transmembrane receptor tyrosine kinase.";

Biochem. Biophys. Res. Commun. 192:1189-1197(1993).

-i- FUNCTION: BINDS AND IS ACTIVATED BY NEURECULINS AND NTAK.

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M29366; AAA35790.1; -.
EMBL; M34309; AAA35979.1; -.
EMBL; S61953; AAB26935.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A36223; A36223.
HSSP; P11362; 1FGK.
Genew; HGNC:3431; ERBB3.
                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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TRANSMEM
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FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
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                                                                                                                                                                                                                                                                                                                                                                                        :: ||||: | |::||||| :| | |||||| :|| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| HAHIVRLGECPGSSLQLVTQYLPGSLDHVRQHRGALGPQLLLNWGVQIAKGMYYLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WMIDSECRPRERELVSEFSRMARDPORFVVIQNEDLGPA---SPLDSTFYRSLLEDDDMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSPSSGY-MPMNQGNLGESCQESAVSGSSERCPRPVSLH-----PMPRGCLASESSEGH
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               VFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AC 06279; Q62955;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DF 15-JUN-2002 (Rel. 41, Last sequence update)
DF 16-CHO-2002 (Rel. 41, Last sequence updat
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R InterPro; IPR000494; EGFR L domain.
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R PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transferase; Tyrosine-Protein; Multigene family; Receptor; Signal; Transferase; Tyrosine-Protein; Multigene family; Receptor; Signal; Transferase; Tyrosine-Protein; Multigene Reminer, Marchalle, Multigene Reminer, Multigene Reminer, Marchalle, Multigene Reminer, Multigene, Mult
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-:- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-:- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES
AND PROMOFIES ITS ASSOCIATION WITH THE PBS SUBUNIT OF
PHOSPHATIDYLINOSITOL 3-KINASE.
-:- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley, TISSUE-Liver;
MEDLINE=96096535; PubMed=8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.;
"Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
Gene 165:279-284(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
                                                                                                                                                                                                                                                                                             REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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ATP (BY SIMILARITY).
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EMBL; U52530; AAC53050.1; -.
HSSP; P11362; 1FGK.
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                                                                                  SEQUENCE FROM N.A
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SEQUENCE OF 959-1078 FROM N.A.
 DVRPQPPSPREGP-----KDVF 1179
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                                                                                                                                                                                                                                          ESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDV 945
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                                           584 HCVNSCPHGILG--AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQ--AEVLMSK
                                                                                                                                                       YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAK
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                             FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                                                                                              MRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEA
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MEDLINE=44350209; Pubmed=8070664;
Clifford R., Schupbach T.;
"Molecular analysis of the Drosophila EGF receptor homolog reveals that several genetically defined classes of alleles cluster in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05). Created)
13-AUG-1987 (Rel. 05). Created)
15-DEC-1989 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (BC 2 7.1.112) (Egfr)
(Gurken receptor) (Torpedo protein) (brosophila relative of ERBB).
EGRR ON TOP OR C-ERBB OR DER OR CG10079.
Eukaryotea, Netazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoc Insecta; Perrygota; Mooptera; Endopterrygota; Diptera; Endopterrygota; Nooptera; Endopterrygota; Diptera; Brachycera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 89:13-16(1997).

-I- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS. CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DOSSO-VENTRAL POLARITIES OF THE COCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTERANCE OF AMMIOSEROSA AND VENTRAL LELL FATES, MAINTERANCE OF AMMIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE.,
UNIFORM EXPRESSION IS SERN IN WING DISKS, GENITAL DISK, ANIAGEN OF
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
AND THORACIC AND ABDOMINAL GANGLIA.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND
                                                                                               SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                        MEDLINE=92038942; PubMed=1936959; Raz E., Schejter E.D., Shilo B.Z.; "Intertallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases."; Genetics 129:191-201(1991).
                                                                                                                                                                                                                                  MEDLINE=97248481; PubMed=9094709;
Perrimon N., Perkins L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
         MEDLINE=8137938, PubMed=2983232; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.; A Drosophila genomic sequence with homology to human epidermal growth factor receptor."; Nature 314:178-180(1985).
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AF109082; AAD26132.1; JOINED.
AF109078; AAD26133.1; -.
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EMBL; AF052753; AAC08536.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF052754; AAC08535.1; -.
AF052752; AAC08535.1; JOINED.
K03054; AAAS1462.1; -.
K03417; AAAS1460.1; -.
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AAD26131.1;
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   STRAIN=Daekwanryeong;
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AF109079;
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                                                                                                                                                                                                                                                                                 EGF receptor
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264 SCTHG-CMGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITEL-----EFAGCKK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 PODKMDKGGE-----CVPCNGPCPKTC-------PGVTVLHAGNIDSFRNCTV 422
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                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000494; EGFR L domain.

R InterPro; IPR000494; EGFR L domain.

InterPro; IPR00019; Euk_pkinase.

R InterPro; IPR001245; Furin-like.

R InterPro; IPR001245; Furin-like.

R InterPro; IPR001245; Furin-like.

R Pfam; PF001039; Propp. L domain; 2.

R PRINTS; PR00109; TYRKINASE.

R PRINTS; PR00109; TYRKINASE.

R PROPOM; PD000001; Euk_pkinase; 1.

R MART; SM00219; TYKC; 1.

R MART; SM00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00110; PROTEIN KINASE TYR; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.

R PROSITE; PS0011; PROTEIN KINASE DOM; 1.

M Transmembrane; Glycoprotein; Receptor; Phosphorylation; Transferase;

M Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing;
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Best Local Similarity 32.6%; Pred. No. 3.9e-95;
Matches 466; Conservative 182; Mismatches 428; Indels 352; Gaps
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EXTRACELLULAR (POTENTIAL).
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ATP (BY SIMILARITY)
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                                         EMBL; X02293; CAA26157.1; EMBL; X789210; CAA55523.1; EMBL; X78918; CAA55521.1; EMBL; X78919; CAA5552.1; PIR, X78919; CAA5552.1; PIR, X78919; CAA5522.1; PIR, X78919; CAA5522.1; PIR, X789; PIR, X189; 
AE003454; AAF46732.1;
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Avian leukosis virus.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11864;
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                             VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
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                                                                                                                                                                                                                               VYKGIWI PDGENVKI PVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTST
                                                                                                                                                                                                                                                                                                          1134 VNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL--
                                                                             PKNKYNDRGVCRECHATCDGCTGPKDTIGIGACTTCNLAIINNDATVKRCLLKDDKCPD-
                                                                                                                                             ECPADHYTDEEORECFORHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTS
                                                                                                                                                                                               KRRQQKIRKYT - - MRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGT
                                                                                                                                                                                                                                                                VQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLV
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                                                                                              SYMPIWKF--PDEEGACQP-----CPI-----
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21-JUL-1986 (Rel. 01, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112) V-ERBB.

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ERBB ALV P00534;

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                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
MISCELLANGOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS AND SUBSEQUENTLY DEVELOP LEUKEMIA: THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIREAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GBNE, WHICH LEADS TO C-ERBB ACTIVATION.
MISCELLANGOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNOAOMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000001; Euk_pkinase; 1.
SMART; SMOG19; TyrKc; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
TABREFEASE; Tyrcsinc-profein kinase; ATP-binding; Oncogene; Glycoprotein; Phosphorylation.
(1) — SEQUENCE FROM N.A. MEDINE-8522822; PubMed=2988784; Milsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Raines M.A., Kung H.-J.; Crittenden L.B., Raines M.A., Kung H.-J.; Processing and promoter insertion result in expression of amino-truncated EGF receptor."; Cell 41:719-726 [1985].
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ATP (BY SIMILARITY).

BY SIMILARITY.

E705E33A0BE01FCC CRC64;
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PIR, B00643; TVFVLV.
HSSP, P11362; IFGK.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR00145; Tyr pkinase.
Pfam; PF00069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
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SIMILARITY: BELONGS
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modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
                                               EMBL; KO2006; AAA42394.1; ALT_INIT.
EMBL; KO1216; AAA42400.1; -.
PIR; A00644; TVYUH.
                                                                                                                                                                                                                   Phosphorylation.
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Matches 354; Conservative
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257
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DOMAIN 13
NP BIND 13
BINDING 16
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CONFLICT
SEQUENCE
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                                                                                                                                         RSILLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEP 1059
                                                                                                                                                                                                                                         1115 PSET -- DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKN 1172
                                                                                                                                                                                                                                                                                           GVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYW 1217
                                                                                                                                                                                        1060 SEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL 1114
                                                                                                                                                                 449
                                                                                                                                                                                                           528 QIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFESSPYW 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYZOBINE PHOSPHATE.
DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K.;
KWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPPI
                                                                                       CTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFY
                                                                                                     CTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERWHLPSPTDSKFY
                                      KWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPARRIPDLLEKGERLPQPPI
                                                                                                                                                   -!- MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H;
MEDLINE-84026539; PubMed-6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima
"The erbB gene of avian erythroblastosis virus is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-152 FROM N.A.

MEDLINE=84223957; PubMed=6128658;
Debuire B., Henry C., Benaissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals
"Sequencing the erbA gene of avian erythroblastosis virus reveals
w type of oncogene.";
Science 224:1456-1459(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                            1218 DQ-----DPPE----RGAPPSTFKGTPTAENPEYLGLDVP 1248
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(See http://www.isb-sib.ch/announce/
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140 S -> F (IN REF. 2).
1- V (IN REF. 2).
67633 MW; 76EBCDD06745D609 CRC64;
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InterPro; IPR001245; Tyr pkinase.
Pram; PP00069; pkinase; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
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PSETDGYVAPLICSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LERAKTLSPGKNG 1173
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      PNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELREATSPKANKE 178
                                                                                                                                                                                                                                                                                               CTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFY 999
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                                               ILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWC
                                                                                                                                                                                                                                                                                                                                                                                                       cell DNA
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01.JAN-1990 (Rel. 13, Created)
01.JAN-1990 (Rel. 13, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (CER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLUIAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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01-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLING=87064458; PubMed=2878164;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythroid cells.";
Mol. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
      ----NTNOSPLAKTVFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                               01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112)
V-ERBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
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PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE TOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene; Glycoprotein; Phosphorylation.
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ATP (BY SIMILARITY).
BY SIMILARITY.
525 -VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-
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                                         1214 LYYWDQDPPERGAPPSTFKGTPTAENPEY 1242
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HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
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54.2%; Pre
tive 63;
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                                                                                  SPYWIQSGNHQ----
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LIYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RWGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
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105; Mismatches 258; Indels 34; Gaps
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                                                                                                                                                                                                                                                             SMART; SMOOJOSI; FU'S TOTELIN KINASE ATP; PARTIAL.
PROSITE; PSOOJO9; PROTEIN KINASE TYR; PARTIAL.
PROSITE; PSOOJO9; PROTEIN KINASE TOM; PARTIAL.
TRANSMEMBARANE; Glycoprotein; Receptor; Signal; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARIT
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                                                                                                                        EMBL; M20386; AAA48760.1; -.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR00194; EUK pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR00145; Tyr pkinase.
Pfam; PP00757; Furin-like; 1.
Pfam; PP01009; Recep_L domain; 2.
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Matches 310; Conservative
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303 PHNYVVTDHGSCVRSCNTDTYEV-EENGVRKCKKCDGLCSKVCNGIGIGELKGILS-INA 360
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                                                                                                                                              PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQY1KANSKFIGI 359
                                                                                                                                                                                                                                                                  419 LPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVH 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PL 182
                                              TLID-TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ
                                                                                       CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
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Search completed: July 22, 2003, 09:17:54 Job time: 16.5911 secs

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July 22, 2003, 08:22:34; Search time 48.3575 Seconds (without alignments) 5347.444 Million cell updates/sec
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6815
1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O18735 Canis famil	O90x70 rattus norv	O9ep98 mus musculu	O9vh40 xiphophorus	O9w6f6 dallus dall	P79754 fugu rubrip	O9bih9 anopheles a	Oguk79 homo sapien	OBr2x1 mus musculu	086712 avian rous-	086714 avian rous-	O8wvv0 homo sanien	064895 avian ervth	085468 avian ervth	O9wvf5 mus musculu	
SUMMARIES	ID	018735	09QX70	86436O 1	1 Q9YH40	09W6F6	1 P79754	09ВІН9	Q9UK79	Q8R2X1	5 Q86712	5 Q86714	OSWYVO	5 Q64895	5 Q85468	O9WVF5	Q9ERV6
	Query Match Length DB	1259 6	1209 11	1210 11	1165 13	1137 13	1328 13	1433 5	419 4	367 11	729 15	567 15	412 4	962 15	545 15	655 11	643 11
ф	Query Match L	90.3	45.4	45.0	39.5	38.8	33.2	29.5	27.5	25.5	25.2	25.2	24.9	24.4	24.1	21.4	21.2
	Score	6152	3096	3067	2692	2646.5	2264	2010.5	1871	1739	1720	1718	1697.5	1662.5	1645	1458.5	1442.5
•	Result	m	7	n	4	ß	9	7	89	6	10	11	12	13	14	15	16

Q9y1x8 ephydatia f	Q23821 caenorhabdi	Q26566 schistosoma	Q90836 gallus gall	Q9ese0 rattus norv	Q14256 homo sapien	Q9psh2 gallus gall	Q923v5 rattus norv	P11776 xiphophorus	Q8szwl drosophila	Q99162 xiphophorus	Ogpvz4 xenopus lae	Q9bud7 homo sapien	Ognivs biomphalari	O9bg66 oryctolagus	093457 scophthalmu	Q8uw85 paralichthy	Q8uw86 paralichthy	Q9u5a8 bombyx mori	073798 xenopus lae	Q8uw84 paralichthy	Q8uw83 paralichthy	Q9qvw4 rattus sp.	Q9ygh8 scophthalmu	Ogvág4 drosophila	Q96135 homo sapien	007912 homo sapien	O54967 mus musculu	
Q9Y1X8	023821	026566	090836	OBSEO	014256	Q9PSH2	Q923V5	P11776	Q8SZW1	099162	09PVZ4	Q9BUD7	SVUNGO	99BG60	093457	Q8UW85	Q8UW86	Q9U5A8	073798	Q8UW84	QBUWB3	Q9QVW4	Q9YGH8	Q9VD94	Q96L35	007912	054967	09UM04
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1193	1368	1717	527	478	165	599	176	346	435	311	1362	331	1671	149	1418	1368	1369	1472	1358	1412	1418	1371	1245	2144	935	1036	1055	1001
18.3	17.3	17.0	15.9	14.0	13.3	13.2	13.0	11.8	11.4	11.1	10.8	10.8	10.7	10.6	10.1	6.6	9.7	6.7	7.6	9.6	9.5	9.5	9.5	9.0	9.8	9.8	9.8	8.6
1250	1178.5	1161	1084	953.5	906	900.5	887	806.5	778	754.5	734.5	734	732	723	069	675.5	629.5	659.5	629	657	644.5	625	624	614.5	589	587.5	587.5	586.5
11	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	2	43	44	45

ALIGNMENTS

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RESULT 1

10 018735

AC 018735

AC 018735

D 01-JUN-1998 (TERMELTE1. 05, Created)

T01-JUN-1998 (TERMELTE1. 05, Last sequence update)

T01-JUN-1998 (TERMELTE1. 05, Last sequence update)

DT 01-JUN-2002 (TERMELTE1. 21, Last annotation update)

Exharyotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OS Canis familiaris (Dog).

C Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Canis.

C Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Canis.

C Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Canis.

NUBL TaxID-9615;

RN NCBL TaxID-9615;

RN P SEQUENCE FROM N.A.

RA Yokota H.;

RY ACORT ACOINING OF ExbB-2 from canine mammary gland.";

EMBL; AB008451; BAA23127.1; ...

BR PSEP; PRO00249; EGFR L domain.

DR InterPro; IPR000249; EGFR L domain.

DR InterPro; IPR001745; Tyr_pkinase.

DR InterPro; IPR001745; Tyr_pkinase.

DR InterPro; PR0004019; Yup_motif.

DR Pfam; PF00100; PR004019; Yup_motif.

DR Pfam; PF00100; PR004019; Vip_motif.

DR Pfam; PF00100; PR0TEIN KINASE DOM; 1.

DR PROSITE; PS00018; EF HAND; UNKNOWN 1.

DR PROSITE; PS00019; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00010; PROTEIN KINASE DOM; 1.

DR PROSI
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Earp H.S.;
"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."; Mol. Cell. Biol. 10:2973-2982(1990)
                                              NOPDVRPOPPSPREGPLPAARPAGATLER----AKTLSPGKNGVVKDVFAFGGAVENPE
                                                                                                                                                                      YLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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SEQUENCE FROM T. L., Earp H.S.;
Guttridge K., Dawson T. L., Earp H.S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M3734; AAF14008.1; -.
RESP; P11362; 1FGK.
RESP; P11362; P11362; 1.
RESP; P11362; P11362; T11362; T11362; 1.
RESP; P11362; P11362; T11362; T11
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MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee
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Last annotation update)
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STRAIN-FISHER; TISSUE-LIVER;
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                                                             MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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 Length 1259;
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 DB
                             45; Mismatches
90.3%; Score 6152;
90.0%; Pred. No. 0;
              Best Local Similarity 90.0%
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28; 61 LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE Gaps

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                                              CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC 299
                                                                                                                              TELE-FAGCKKIFGSLAFLPESFDGDPASNTAPQYIKANSKFIGITELTGYLYISAWPDS 418
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                                                                                                                      PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQY1KANSKFIGI 359
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            LIYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD
                                                                 TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ
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                                                                                                                                                                                                           PEYLNTAQ------PTCLSSGFDSSALWIQKGSHQMSLDNPDYQQDFFPKEAKPNGI 1185
                                 STRAIN=C3H/101, 129/SvJ, AND 129/SvEvTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
Maihle N.J.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275366; AAG28045.1;
EMBL; AF275364; AAG28045.1; JOINED.
EMBL; AF275364; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; JOINED.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Egptermal growth factor receptor isoform 1.
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MGD; MG195294; EGFK.
INTERFYC; IPR000494; EGFR_L domain.
INTERFYC; IPR000719; EUK, PKINASE.
INTERFYC; IPR001249; FUTIN-like.
INTERFYC; IPR001249; TYT, PKINASE.
INTERFYC; IPR001249; TYT, PKINASE.
FFAM: PF00057; FUTIN-like; 1...
FFAM: PF00057; FUTIN-like; 1...
FFAM: PR00109; PKINASE; 1...
FMART; SM00020; STKC; 1...
SWART; SM00020; STKC; 1...
SWART; SM00020; STKC; 1...
SWART; SM00020; STKC; 1...
PROSITE; PS00109; PROTEIN_KINASE DAP; 1...
PROSITE; PS00109; PROTEIN_KINASE_TY; 1...
PROSITE; PS00109; PROTEIN_KINASE_TY; 1...
PROSITE; PS00109; PROTEIN_KINASE_TY; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1210 AA
                                                                                                                                                                                                                                                                                                                   ||| ||||| ||| : |
FKG-PTAENAEYLRVAPP 1202
                                                                                                                                                                                                                                                                          FKGTPTAENPEYLGLDVP 1254
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Db 956 DADSRPKFRELILEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMEDVVDA 1015 1021 EEYLVPQQGFFCPDPAPGAGGMVHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080 1016 DEYLTPQQGFF	RESULT 4 09YH40 ID 09YH40 DY 109YH40 DY 10-WAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 15, Last sequence update) DT 01-OCT-2000 (TrEMBLrel. 21, Last annotation update) DT 01-OCT-2000 (TrEMBLrel. 21, Last annotation update) DT 01-Graphorus xiphidium. SXIPADPOPORUS XIPADPOPORUS XIPADPOPORUS (Created) CC XIPADPOPORUS XIPADPOPORUS (Created) CC Cyptinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; CC Cyptinodortiformes; Poeciliidae; Xiphophorus. CC Cyptinodortiformes; Poeciliidae; Xiphophorus Albinitrijevic. N., Winkler C., Wellbrock C., Gomez A., Duschl J., RA Altschmied J., Schartl M.; CD COCORD (Created) CC COMED COCORD (Created) CC COCORD (Cre	RN (2) RN SEQUENCE FROM N.A. RA SCHARLIN; Schartl M.;
ATP-binding; Receptor; Transferase. SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64; SQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64; SQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64; SEQUENCE 120 AS; Score 3067; DB 11; Length 1210; Gaps 25; Matches 629; Conservative 164; Mismatches 368; Indels 112; Gaps 25; Astches 629; Conservative 164; Mismatches 368; Indels 112; Gaps 25; Astches Gaps Gap	Qy 244 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY 303 Db 240 CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGRYSFGATCVKKCPRNY 299 Qy 304 LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE 363 :	0.03 0.04 0.05

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1010 EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
                                                                                                                                                                             1129 APLTCSPQPEYVNQPDVRPQP-----PSPRE-----GPLP-AARPAGATLERAKTLSP 1175
                                                                                                                                                                                                                                                                                              1106 NONSL---PLVSSGSMDDPDY---QAG-----YQAAF-----LPQTGALTG 1140
                                                                                                                                     161 LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC 220
                                                                                                                                                                                                        1070 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
                                                                                                                                                                                                                                                         GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                             Query Match 38.8%; Score 2646.5; DB 13; Length 1137; Best Local Similarity 46.4%; Pred. No. 9.6e-191; Matches 529; Conservative 173; Mismatches 359; Indels 79; (
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MEDLINE=99263203; PubMed=10328884;
Dixon M., Lumsden A.;
"Distribution of neuregulin-1 (nrg1) and erbB4 transcripts
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1137 AA.
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR00174; Furin-like.
InterPro; IPR001745; Furin-like.
InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR00129; YuP moif.
Pfam; PF00757; Purin-like; I.
Pfam; PF00757; Purin-like; I.
Pfam; PF00757; Purin-like; I.
Pfam; PF00705; Pirinase; I.
Pfam; PF00705; Pirinase; I.
ProDom; PR00109; TYRKINASE.
ProDom; PR00109; TYRKINASE.
ProDom; PR00109; TYRKINASE.
PROSTITE; PS00107; PROTEIN KINASE DOM; I.
PROSTITE; PS00107; PROTEIN KINASE DOM; I.
PROSTITE; PS00109; PROTEIN KINASE TYR; I.
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Mol. Cell. Neurosci. 13:237-258(1999)
EMBL; AF121963; AAD31764.1;
HSSP; P11362; IFGK.
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                                                                                                                                                                                                                  VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK 175
                                                                                                                                                                                                                                                                                              CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCNEHCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAA 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 VIMWWPENMTSLSVFQNLEIIRGRTTFSRGFSFVVVQVSHLQWLGLSSLKEVSAGNVILK 467
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                                                                                                                                                                                                                                                                                                                                                                              SCHYDRGGRCYASCNLLQGEPREAQYDGRCYQCHQECLVQTDSLTCYGPGPANCSKCAH
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                                                                             148;
                                    Length 1165;
                                                                           Indels
1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
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llarity 45.3%; Pred. No. 3.7e-194;
Conservative 163; Mismatches 387;
                                Query Match
Best Local Similarity
Matches 578; Conserv
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SEQUENCE
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(TrEMBLrel.
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SEQUENCE 1328 AA; 148
                                           PRELIMINARY;
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01-JUN-2002 (
ErbB3.
                                                          01-MAY-1997
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                                                                   QLEHNHNAKYTYGAFCVKKCPHNFV-VDSSSCVRACPSSRMEV-EENGIRMCKPCTDICP
                                                                                                                                                                     KQISAGNIYITDNSNLCYXHTVMWTSLFSTPSQKTVIHRNKKAENCTADGMVCNELCSSD
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                                                                                                                                                                                                                                                                                                     GPLPAA-RPAGATLERAKTLSPGKNGVVKDVF-----AFGGAVENPEYLTPQGGAAP
RVCYGLGMQYIKANSKFIGITELE-FAGCKKIFGSLAFLPESFDGDPASNTAPQYIKANS
                                                                                                    239 IFQTVREITGYLNIQSWPENMTDFRVFSNLVTIGGRALYSGLSLLILKQQGITSLQFQSL
                                                                                                                                                                                            519 HCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCF
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                                                                                                                                                                                                                             GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF
                                  AEOCDGRCYGPYVSDCCHRECAGGCSGPKDTDCFACMPINDSGACVTOCPOTFVYNPTTF
                                                         ESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCA
                                                                                                                          399 KFIGITELTGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSL
                                                                                                                                                           RELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YPKDG--PSGLNQLGLMNLTEILDGGVQIINNKYLRYGPWYYWRDII-RNNDAPIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCKGPLDTDCFACRLFNDSGACVPQCPQTLIYNKQTFQMETNPNAKYQYGSICVSQCPT
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                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Edrinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99177347; PubMed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA around the wnt1 locus of rubripes.";
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                                                                                                                                                                       (TrEMBLrel. 03, Created)
(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.0%; Pred. No. 9.3e-162; Matches 515; Conservative 155; Mismatches 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.2%; Score 2264; DB 13; 40.0%; Pred. No. 9.3e-162;
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InterPro; IPR000719; Euk Pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro: IPR001245; Tyr pkinase.
Pfam; PF00059; pkinase; 1.
Pfam; PF00069; pkinase; 1.
ProDom; PP000001; Euk Pkinase; 1.
SWART; SW00261; FU; 3.
SWART; SW00261; FU; 3.
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EMBL; AF056116; AAC34391.1;
HSSP; P11362; 1FGK.
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Local Similarity
                              SEQUENCE FROM N.A
  Anopheles.
NCBI_TaxID=7165;
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                                                                                                                                                                                                                                                                                      890
                                                                                                                                                                                                                                                                                                                           ARCPSGUKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA 657
                                                                                                                                                                                                    OMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE 770
                                                                                                                                                                                                                                                        LLSMGSLDHPYIVRLIGICPGTCLQLVTQLSSHGSLLEHIRQHKTSLDPQRLLAWCVQIA 917
                                                                                                                                                                                                                                                                                                ----GILIKRROOKIRKYTMRRLLQETELVEPLTPSGAMPNQA
PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
          VNWTQLFRGSRVRANSLNSNRPMAECVADGRVCDPLCSDSGCWGPGPDQCLSCRNYSRHG
                                                                             ECVEECRVLQGLPREYVNARH-CLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
                                                                                           TCVAGCHFNSGIPREFAGLNGVCVACHPECKPQTGKASCTGPGADECMACTKFRDGPYCM
                                                                                                                                 SCCPAGVN-DGEKGLIFKFPNREGHCEPCHQNCTQGCSGPGLNDC---LEAARLTISSGQ
                                                                                                                                                                          771 AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
                                                                                                                                                                                                                                                                                    KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMA
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                                       VPWDQLFRNPH-QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GLGDRFATPSLQPSPSWSTSPSQINSYMVMTQLRYD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09BIH9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 DQSFDGFQQVYTNFSFGPRYIKIDPDRLEVFSTVKEITGFINIQAHPNFTTLNYFRNLE 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 471; Conservative 195; Mismatches 396; Indels 385;
                                          gambiae
Lycett G. J.;

Lycatus G. J.;

"Cloning, expression and localisation of the Anopheles gamb bydearmal growth factor receptor.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ301655; CAC35008.1; -...

R HSSP; Pli362; 1PGK.

R InterPro; 1PR0001345; CytC, heme bind.

InterPro; 1PR0001345; CytC, heme bind.

InterPro; 1PR0001345; CytC, heme bind.

InterPro; 1PR000134; EUK, PATIANSE.

R InterPro; 1PR001230; EUK, PATIANSE.

R Pfam; PF001030; Recept. domain; 2.

R Pfam; PF001030; Recept. domain; 2.

R PRNOST; SM00129; TYRKINASE.

R SMART; SM00129; TYRKINASE.

R SMART; SM00129; TYRC; 1.

R SMART; SM00129; TYRC; 1.

R SMART; SM0011; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE TYR; 1.

R PROSITE; PS00101; PROTEIN KINASE TYR; 1.

R PROSITE; PS00101; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                            on G.M.;
a secreted
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Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.I Submitterd (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF177761, AADS609.2; ---
InterPro: IPR000494; EGFR L. domain.

InterPro: IPR00174; Furin-like.

Pfam; PF00757; Purin-like; 1.

Pfam; PF01030; Recep_L_domain; 1.

SMART; SM00261; FU; 1.

SEQUENCE 419 AA; 45472 MW; FECIBE347E2D030C CRC64;
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                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99415911; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.
"The HER-2/neu receptor tyrosine kinase gene encodes a secrei autoinhibitor.";
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                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
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98.8%; Pred. No. 7.8e-133;
iive 1; Mismatches 3;
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Best Local Similarity 98.8'
Matches 341; Conservative
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                         SLPRLYSVDSKTCGDCHQECKD----FCYGPNEDNCGSCMNVKDGRFCVAECPTTKHAM
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GLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP -
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                   254 RRLLQERELVEPLTPSGEAPNQAHLRILKETEFKKVKVLGSGAFGTVYKGLMIPEGEKVK 313
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      PONGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
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MEDLINE=94203659; PubMed=8152791;

Wennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak Johnsson A., Beug H.;

"Retroviral capture of c-erbB proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbB genes different transforming capacities.";

Oncogene 9:1307-1320(1994).

EMBL; 869372; AAC66727.1; -.
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
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InterPro; IPR001245; Tyr pkinase.
Edm; PF00069; pkinase; I.
PRINTS; PR00109; TYRINASE.
ProDom; PD000001; Euk_pkinase; I.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                             1129 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG 1188
                                                                                                                                                                                                                                                                                                                                                      1189 GAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEY 1248
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                                                                                                                                    61 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPSSPMDSTFYRSL
                                                                           1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                   949 IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                            LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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MEDLINE=94201859; PubMed=8152791;

Wennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
Johnsson A., Beug H.;

"Retroviral capture of c-erbB proto-oncogene sequences: rapid
evolution of distinct viral genomes carrying mutant v-erbB genes with
different transforming capacities.";
                                 Gaps
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 Length 367;
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InterPro; IPR004028; Retro M.
InterPro; IPR004028; Retro M.
InterPro; IPR00145; Tyr_Ekinase.
Féam; PF00069; Pkinase; 1.
PF000m; PD000001; Buk pkinase; 1.
PF000m; PR00107; PR0TEIN KINASE ATP; 1.
PR0SITE; PS00107; PR0TEIN KINASE DOM; 1.
PR0SITE; PS00109; PR0TEIN KINASE DOM; 1.
PR0SITE; PS00109; PR0TEIN KINASE TYP; 1.
                                33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avian rous-associated virus type 1.
Viruses, Retroid viruses, Retroviridae, Alpharetrovirus.
NCBI_TaxID=11950,
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Last sequence update)
Last annotation update)
   DB 11;
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; Score 1739; DB 11;
; Pred. No. 5.9e-123;
11; Mismatches 33;
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 25.5%;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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                             Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 54.8
Matches 358; Conservative
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                Similarity
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Best Local
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1129 APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG 1188
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MEDLINE=90206603; PubMed=1869616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
Examino acids from the retroviral gene gag greatly enhance the
transforming potential of the oncogene v-erb-B.";
Oncogene 5.15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL, X52209; CAA36459.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag,v-erb-A,v-erb-B protein.
GAG,V-ERB-A,V-ERB-B.
Avian erythroblastosis virus.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                      cell
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                                                                                                                                                                                                                                                                                             53;
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Wan D.F., Gu J.R.;
"Novel human cDNA clones with function of inhibiting cancer
growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 WVWTCQCEPEGQVRRSPDVSSGSREGLTSAGIKRWEGPPTTSRGTCHARN
                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF318349; AAL55856.1;
InterPro; IPR002048; EF-hand.
InterPro; IPR001945; Tyr_pkinase.
InterPro; IPR001945; Tyr_pkinase.
InterPro; IPR00419; YLP_motif.
Pfam; PF0069; pkinase; Ţ.
Pfam; PF0069; pkinase; Ţ.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SMO0219; Tyrkc; 1.
SMART; SMO019; Tyrkc; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                24.9%; Score 1697.5; DB 4, 80.5%; Pred. No. 9.6e-120; ive 5; Mismatches 22;
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                                                                                                                                                                                            GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
                                                                                                                                                                                                                                                                                                         ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                 Indels 102;
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                                                                                          567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
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Catarrhini; Hominidae;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                25.2%; Score 1/10; ___
55.4%; Pred. No. 4.4e-121;
tive 73; Mismatches 112;
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     SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS50011; PROTEIN KINASE DOM;
PROSITE; PS00109; PROTEIN KINASE TYR;
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                   Best Local Similarity 55.49
Matches 357; Conservative
                                                              Tyrosine-protein kinase.
NON TER
SEQUENCE 567 AA; 63390
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SEQUENCE FROM N.A.
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DAR WEEK WAS A STANFORD TO BE A STANFORD

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RDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGA 1039
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RX MEDINE-88217326; PubMed=2897102;
RX MEDINE-88217326; PubMed=2897102;
RX Gotting P., Vennetrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
Common site of mutation in the erbB gene of avian erythroblastosis ricomnon site of mutation in the erbB gene of avian erythroblastosis.

RI Gordene Res. 1:265-278(1987).
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                                                                                                                                                                                          ITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              085468;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1160 ARPAGAT-LERAKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
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R PRINTS; PR00147; STROIDFINGER.

R Probom; PD000001; Euk_pkinase; 1.

R Probom; PD00159; Znf_C4steroid; 1.

SMART; SM00430; HOLI; 1.

R SMART; SM00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R SMART; SM0031; NUGLEAR RECEPTOR; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TOR; 1.

R PROSITE; PS00119; PROTEIN_KINASE_TOR; 1.

R PROSITE; PS00119; PROTEIN_KINASE_TOR; 1.

R PROSITE; PS00119; PROTEIN_KINASE_TOR; 1.

M ATP-binding; DNA-binding; Nuclear protein; Rinase; 1.

M Transcription regulation; Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.4%; Score 1662.5; DB 15; Length 962; Best Local Similarity 39.7%; Pred. No. 1.5e-116; Matches 420; Conservative 115; Mismatches 253; Indels 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
EMBL, X52211; CAA36459.1; JOINED.
HSSP; P10828; ZNLL.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR00173; Stdhrmn receptor.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR01245; Tyr pkinase.
InterPro; IPR01628; Znf C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00104; pkinase; 1.
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SEQUENCE
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Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
SMART: SM00261; FU; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001)
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                                                                                                      YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
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                       LDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
                                                                                                                                                             LGSQDLLNWCMQ1AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CSTBL/63; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
Maihle N.J.,
"Alternative Transcripts from the Human and Mouse EGFR Genes Encode
Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor
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Sciurognathi, Muridae, Murinae, Mus
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524 LPMDSRYQN-----SHSTAVDNPEYL 544
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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C STRAIN=C57BL/6J; TISSUE=LIVER;

K MEDLINE=21085660, PubMed=11217851;

K Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Salto R.,

Kadota K., Matsuda H.A., Ashburar M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburar M., Radalov G., Quackenbush J.,

Rochiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ruschincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sasamoto N.,

Sasaki H., Sato K., Schoenbach C., Seyar T., Shibata Y., Storch K.-F.,

Nymishaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nanahiaria H.,
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EMBL, AF275366; AAG28047.1; -.
EMBL, AF275364, AAG28047.1; JOINED.
EMBL, AF275365; AAG28047.1; JOINED.
EMBL, AK004944; BAB23688.1; -.
EMBL, AK004983; BAB23641.1; -.
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Search completed: July 22, 2003, 09:01:11 Job time : 53.3575 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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SEQ4-369-383-12 6815 1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

SUMMARIES

		Description	P04626 homo sapien	P06494 rattus norv	Q60553 mesocricetu	P00533 homo sapien		Q15303 homo sapien	Q62956 rattus norv	P13388 xiphophorus			P04412 drosophila	P00534 avian leuko		avian			P70424 mus musculu	002466 branchiosto	P15127 rattus norv	Q25410 lymnaea sta	P15208 mus musculu	P06213 homo sapien	Q9wtl4 mus musculu			P14617 cavia porce	homo a			P24062 rattus norv	P09208 drosophila	92	P07949 homo sapien
SUMMARIES		ΩI			ERB2_MESAU		EGFR_MOUSE	ERB4 HUMAN	1 1	XMRK_X I PMA		ERB3_RAT		ERBB_ALV	ERBB_AVIER	ERBB_AVIEU	EGFR_CHICK	LT23_CAEEL	ERB2_MOUSE	ILPR_BRALA	INSR_RAT	MIPR_LYMST	INSR_MOUSE	INSR_HUMAN	IRR_MOUSE	IRR_HUMAN	HTK7_HYDAT	IRR_CAVPO	IG1R_HUMAN	INSR_AEDAE	IG1R_MOUSE	IG1R_RAT	INSR_DROME		RET_HUMAN
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d		Match	97.6	9	•	45.4	•		42.6	38.9	34.9	33.8	28.2	25.7	25.0	23.9	22.8	18.7	16.8	10.7	10.2	10.2	10.2	10.2	10.1	10.0	6.6	9.9	•	9.5	•		9.0	80	9.
		Score	6653	5865	5851.5	3095	3070	2919.5	2900	2652.5	2375.5	2303.5	1922	1749.5	1703	1630	1553	1275	1142.5	730	969	969	695.5	695	689	682	929	674.5	644	627		622.5	612	665	588
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ALIGNMENTS

PRT; 1255 AA. sed) sequence update) sinase erbB-2 precursor (EC 2.7.1.112) sgene) (C-erbB-2) (Tyrosine kinase-type cell 7, 19). s; Craniata; Vertebrata; Euteleostomi;	d=3003577; Akiyama T., Semba K., Nomura N., Miyajima N., encoded by the human c-erb-B-2 gene to receptor:";	SEQUENCE FROM N.A. MEDLINE=86070181; PubMed=2999974; Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., Coussens L., Yang-Feng T.L., Libermann T.A., Schlessinger J., McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J., "Tyrosine kinase receptor with extensive homology to EGF receptor "Tyrosine kinase receptor with neu oncogene."; Science 230:1132-1139(1985)	SEQUENCE OF 737-1031 FROM N.A. MEDLINE=86016729; PubMed=2995967; Semba K., Kamata N., Toyoshima K., Yamamoto T.; Semba K., Kamata N., Toyoshima K., Yamamoto T.; "A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary gland adenocarcinoma."; Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985). [4] VARIANTS VAL-654 AND VAL-655.	MEDLINE-93194196; PubMed-8095488; Bheani A., Low J., Wallace R.B., Wu A.M.; "Characterization of a new allele of the human ERBB2 gene by allele-specific competition hybridization."; Genomics 15:45-428(1933). -!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POPERTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF- ALPHA AND AMPHIREGULIN. -!- CATALYIT ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate. -!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS -!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS -!- SUBCELLULAR. LOCATION: Type I membrane protein.
HUMAN STANDARD; PR: ERB2 HUMAN STANDARD; PR: ERB2 HUMAN STANDARD; PR: 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last seques 15-JUN-2002 (Rel. 41, Last annote Receptor protein-tyrosine kinase (PlaSerbB2) (Rub proto-oncogene) surface receptor HER2) (M.N. 19). ERBB2 OR HER2 OR NGL OR NGL. Homo sapiens (Human). Homo sapiens (Human). Homo sapiens (Human). Amanalia, Eutheria; Prinates; Carmanalia, Eutheria; Prinates; Carmanalia; Prinates; Carmanalia; Prinates; Carmanalia; Eutheria; Prinates; Carmanalia; Prinates; Prinates; Carmanalia; Prinates; Prinates	NCBI_TaxiD=9606; SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=86118663; PubMed=3003577; MEDLINE-86118663; PubMed=3003577; Sato T., Ikawa S., Akiyama T., Saito T., Toyoshima K.; "Similarity of protein encoded by teptdermal growth factor receptor."; Nature 319:230-234(1986).	SEQUENCE FROM N.A. SEQUENTE FROM N.A. COUSSENS L., Yang-Feng T.L., Liao Y.C., McGrath J., Seeburg P.H., Libermann T.A Francke U., Levinson A., Ullrich A.; "Tyrosine kinase receptor with extensive shares chromosomal location with neu ons Science 230:1132-1139(1985).	SEQUENCE OF 737-1031 FROM N.A. MEDLINE=86016729, PubMed=2995967; "A v-erbB-related protooncogene, c- c-erbB-1/epidermal growth factor-re human sallvary gland adenocarcinoma Proc. Natl. Acad. Sci. U.S.A. 82:64 [4]	MEDLINE-93194196; PubMed-8095488; Bhania A., Low J., Wallace R.B., Wu A Ehania A., Low J., Wallace R.B., Wu A specific competition of a new allele of specific competition hybridization."; Genomica 15:424-429(1939). -I- FUNCTION: ESSENTIAL COMPONENT OF ALTHOUGHT NEUREGULINS DO NOT INTER POTENTIAL LIGAND FOR THIS RECEPTO POTENTIAL LIGAND FOR THIS RECEPTO ALPHA AND AMPHIREGULIN. -I- CATALYTIC ACTIVITY: ATP + a prote tyrosine phosphate. -tyrosine phosphate. -tyrosine phosphate. -tyrosine phosphate. -tyrosine phosphate. -tyrosine phosphate. -tyrosine phosphate.
RESULT 1 ERB2 HUMAN AC P04626; DT 13-AUG-1987 (Rel. 05 DT 13-AUG-1987 (Rel. 05 DT 15-AUG-1987 (Rel. 05 DE P18-ERB2 HUMAN DE Receptor protein-tyr DE RESERVEN: 41 DE RES	NCBI_TaxID=9606; SEQUENCE FROM N.A. MEDLINE=86118663; PubMed= Admannco T., Irawa S., Ak Salto T., Toyoshima K.; "Similarity of protein en epidermal growth factor r Nature 319:230-234(1986).	SEQUENCE FROM MEDLINE=86070 COUSSEND L., S. McGrath J., S. Francke U., I. Tyrosine kin Shares chromc Science 230:1[3]	SEQUENCE OF 7 MEDLINE=86016 Semba K., Kan "A v-erbB-rel c-erbB-1/epic human salivar Proc. Natl. A (4)	MEDLINE=9319419 Bhani A., Low "Characterizati specific compet Genomics 15:426 -!- FUNCTION: E ALTHOUGHT N ALPHA AND A -!- CATALYTIC A tyrosine ph -!- SUBUNIT: HE (POTENTIAL) -!- SUBCELLULAR
RESULT ERB2 HH ID BAC DT 113 DT 113 DE RG DE RG OS HG OC BR	O R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	\$

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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012. SIMILARITY: BELONGS TO THE EGF RECEPTOR PAMILY.
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SWART; SMO0261; FU; 3.
SWART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE DOW; 1.
Transmembrane; Glycoprofein; Multigene family; Receptor; Signal;
Transmembrane; Glycoprofein; Multigene family; Receptor; Signal;
   : LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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InterPro: IPR00219; Euk pkinase.
InterPro: IPR002145; Purin-like.
InterPro: IPR001245; Tyr pkinase.
InterPro: IPR004019; Yup motif.
Pfam; PF00059; pkinase; I.
Pfam; PF00057; Furin-like; I.
Pfam; PF001030; Recep L domain; 2.
Pfam; PF02757; YLP; Z.
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EMBL, M11761, AAA35808.1;
EMBL, M11762, AAA35808.1; JOINED.
EMBL, M11763, AAA35808.1; JOINED.
EMBL, M11764, AAA35808.1; JOINED.
EMBL, M11764, AAA35808.1; JOINED.
EMBL, M11766, AAA35808.1; JOINED.
EMBL, M11730, AAA75808.1; JOINED.
EMBL, M11206, AAA35808.1; JOINED.
EMBL, M12036, AAA35808.1; -
EMBL, X03363; CAA27060.1; -
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HSSP, P11362, IFGK.
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                                        YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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"The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p185erbB) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor receptor-related protein).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"An extended family of protein-tyrosine kinase genes differentially
expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
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MEDLINE=92155181; Pubmed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak
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MEDLINE-91222560; PubMed=2025425;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                "Three dimensional structure of the transmembrane region of the proto-oncogenic and oncogenic forms of the new protein."; EMBO J. 11:43-48(1992).
                                                                                                                                                                                         LYFOSINE PHOSPHATE.

USUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.

THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.

SUBCELLULAR LOCATION: Type I membrane protein.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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EXTRACELLULAR (POTENTIAL).
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PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Pransferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Proto-oncogene; Disease mutation.
                                                                             -i- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
Crumpton M.J., Sternberg M.J.E., Campbell I.D.
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-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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PIR; A24562; TVRTNU.
HSSP, P11362; 1FGK.
INCEPPO; 1FR000494; EGFR L domain.
INCEPPO; IPR000719; EUK DKINGS.
INCEPPO; IPR001214; FULIN-like.
INCEPPO; IPR001245; TYL_DKINGS.
INCEPPO; IPR001245; TYL_DKINGS.
INCEPPO; IPR00145; TYL_MOLIF.
PÉGM; PF00757; PULIN-like; 1.
PÉGM; PF00757; FULIN-like; 1.
PÉGM; PF02757; YLP; Z.
PRODDM; PD000001; BUK DKINGSe; 1.
SWART; SM00261; FU; 3.
SWART; SM00261; TYLKC; 1.
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MEDLINE=94193007; PubMed=7908275;
MARAMILA T., UShijima T., Ishizaka Y., Nagao M., Arai M.,
Namazaki Y., Ishikawa T.;
"Cloning and activation of the Syrian hamster neu proto-oncogene.";
Gene 140:251-2551994).
-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-I- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbb-2 precursor (EC 2.7.1.112)
Resocricetus auratus (Golden hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butherla; Rodentia; Sciurognathi; Muridae; Cricetinae;
NEBL TaxID=10036; POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY PRT; 1254

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(See http://www.isb-sib.ch/announce/
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RECEPTOR KINASE.

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PROSITE; PSO0109; PROTEIN KINASE TYR; 1.
PROSITE; PSS0011; PROTEIN KINASE DOW; 1.
Transmembrane; Glycoprocein; Multigene family; Receptor; Signal;
Proto-oncogene; Dysease mutation; Proto-oncogene; Disease mutation.
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 entities requires a license agreement ( or send an email to license@isb-sib.ch)
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Pfam; PF00157; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
Pfam; PF02757; YLP; 2.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 3.
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InterPro; IPR000719; Euk pkinase.
Interpro; IPR00174; Purin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP_motif.
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                                                                                                           MEDLINE=21100872; PubMed=11161793; Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balagubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                   POD5.33; PO6268; Q14225; Q9UMD7; Q9UMD8; Q9UMG5; Q92795; O00732; Q90688; Q9B2S2; Q9H2C9; Q9GZX1; Q9H3C9; Q1-JUL-1986 (Rel. 01, Created) C1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor ECR OR ERBB1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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A.J. 8 b. alternative transcript from the human epidermal growth
factor receptor gene encodes a truncated form of the receptor.";
Nucleic Acids Res. 24:4050-4056(1996).
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"Expression of a truncated epidermal growth factor receptor-like
protein (TEGFR) in ovarian cancer.";
Gynecol. Oncol. 65:36-41(1997).
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Lampland.A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
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MEDLINE=97078686; Pubmed=8918811;
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TISSUE=Placenta;
MEDLINE=97256547; Pubmed=9103388;
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MEDLINE=95382957; PubMed=7654368;
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mouse alternative EGFR transcr
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MEDLINE-85270438; PubMed-2991899;
MEDLINE-85270438; PubMed-2991899;
Ishli S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
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Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
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Mroczkowski B., Mosig G., Cohen S.;
ATP-stimulated interaction between epidermal growth factor receptor
and supercoiled DNA.";
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                                                                                                                                                                                                                                            Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
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amplification and three related messenger RNA products in A431
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Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G., O'Malley B.W.;
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Biochem. Biophys. Res. Commun. 124:125-132(1984).
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BELLINE-84245835; PubMed-6-3130563;
Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., I
Roe B.A., Merlino G.T., Pastan I.;
"Human epidermal growth factor receptor cDNA is homologous variety of RNAs overproduced in A431 carcinoma cells.";
Nature 309:806-810(1984)
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J. Biol. Chem. 266:1746-1753(1991).
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MEDLINE=84196372; PubMed=6326261;
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"Disulfide bond structure of human epidermal growth factor receptor.";
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-!- FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.

-!- FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                             ASN-603.
MEDLINE=20198209; PubMed=10731668;
Sato C., Kim J.-H., Abe Y., Salto K., Yokoyama S., Kohda D.;
Sato C., Kim H., Abe Y., Salto K., Yokoyama S., Kohda D.;
"Characterization of the N-01igosaccharides attached to the atypical
"Characterization of the N-01igosaccharides attached to the atypical
ASN-X-Cys sequence of recombinant human epidermal growth factor
**RECEDTOR:";
                                    MEDLINE=96198132; PubMed=8962717; Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.; Manlysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster
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  ASN-175; ASN-413; ASN-444 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/truncated isoform/TEGFR, 3/p110 and 4; are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
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MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568
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PubMed=9556602;
CARBOHYDRATE-LINKAGE SITES ASN-128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87297456; PubMed=3039909; Carpenter G.;
                                                                                                                                           Growth Factors 13:121-132(1996).
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U48725; AACS0797.1; -.
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LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN

Pred. No. 2.7e-157;

Conservative 171;

Local Similarity nes 627; Conserv

Best Loca Matches

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Indels 108;

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1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TP 1199
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Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!* FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                ----DP-----PERGAPPSTFKGTPTA
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STRAINE B6/CJ: TISSUE=Liver;
STRAINE B6/CJ: TISSUE=Liver;
MEDLINE=94170996; PubMed=8122555;
Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
Jenkins N.A., Lee D.C.;
"The mouse waved-2 phenotype results from a point mutation in the EGF
receptor tyrosine kinase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUB=Liver; MEDLINE=93026370; PubMed=1408137; MADLINE=93026370; PubMed=1408137; Mayon B.; Skorecki K.; Yayon B.; Givol D.; Promoter region of the murine fibroblast growth factor receptor 2 (bek/KGFR) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112).
EGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
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STRAIN=BALB/c, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93126380; PubMed=7678348;
Paria B.C., Dass S.K., Andrews G.K., Dey S.K.;
n mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                OGGAAPQPHPPPAFSPAFDNLYYWDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91232866; PubMed=2030916;
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STRAIN=BALB/c; TISSUE=Liver;
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Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes Dev. 8:399-413(1994).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of cell DNA
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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MGD; MGI 95294; Egfr. L domain.

InterPro; IPR000194; Eur L domain.

InterPro; IPR000194; Eur L domain.

InterPro; IPR001194; Furin-like.

InterPro; IPR001194; Furin-like.

InterPro; IPR001194; Furin-like.

R Pfam; PF00157; Furin-like; 1.

R Pfam; PF001000; Euk Dixinase; 1.

R Probom, PD000001; Euk Dixinase; 1.

R SMART; SM00219; Tyrc; 1.

R SMART; SM00219; Tyrc; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

Transmembrane; Glycoprotein; Receptor; Signal; Transferase;

Transmembrane; Glycoprotein; Receptor; Signal; Transferase;

Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
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EPIDERMAL GROWTH FACTOR RECEPTOR.
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1092 YVNQ-SVPKRPAGSVQNPVYHNQPLHP-----APGRDLHYQN--PHSNAVGNPEYLN 1140
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     DSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                                                                                              EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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                                                                                          VHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTH
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TISSUE=Breast carcinoma;
MEDLINE=9189574; PubMed=3833326;
Plowman G.D., Culouscou J.-M., Whitney G.S., Green J.M., Carlton G.W.,
Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HRR4/pl80erb84, a fourth member of the
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                                                                                                                                                                                                                                                                1081 AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPE
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
(p100erbB4) (Tyrosine kinase-type cell surface receptor HER4).
ERBB4 OR HER4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97476287; PubMed=9334263;
Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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J. Biol. Chem. 272:26761-26768(1997)
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   (BY SIMILARITY)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
ERBB4 OR TYRO-2.
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MEDLINE=98221155; PubMed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han
                           GVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGC
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SECUENCE OF 131-199 FROM N.A.

RX SECUENCE OF 131-199 FROM N.A.

RX Carcoll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RA Carcoll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RA Carcoll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RA Carcoll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RA Carcoll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

RT Expression Willer M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

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REMBL; U5251; AACS3037; Euk_pkinase.

RICEPPC; IPR000149; Euk_pkinase.

RICEPPC; IPR00145; YLP_motif.

REMB; PF00069; PK108e; 1.

REMB; RMAR; SM0021; TYRKINASE.

REMART; SM0021; TYRKINASE.

REMART; SM0021; TYRK; 1.

REMART; SM0021; TYRK; 1.

REMART; RM0021; TYRKINASE DOM; 1.

REMART; RM00219; PROTEIN KINASE DOM; 1.

REMART; RM0019; PROTEIN KINASE DOM; 1.

REMOSITE; PS00109; PROTEIN KINASE, TYP; 1.
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                                                                                                                                                                                                                                                                     Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially
expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
                         "Neuregulins promote survival and growth of cardiac myocytes.
Persistence of ErbB2 and ErbB4 expression in neonatal and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                    Biol. Chem. 273:10261-10269(1998)
                                                                                                                                                                    SEQUENCE OF 848-901 FROM N.A.
TISSUE-Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
Lai C., Lemke G.;
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CYTOPLASMIC (POTENTIAL)

357 IGITELEPAGCKKIFGSLAFLPESFDGDPASNTAPQYIKANSKFIGITELTGYLYISAWP 417 DSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 419 DSSNIDKFINCTKINGRLILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 410 PHATPAPADOLERNPHQALLHTANREPEDECVGEGLACHQLCARGHCWGPGFTQCVNCSGPLR 417 VHYVPWDQLFRNPHQALLHTANREPEDECVGEGLACHQLCARGHCWGPGFTQCVNCSGPLR 417 VHYVPWDQLFRNPHQALLHTANREPEDECVGEGLACHQLCARGHCWGPGFTQCVNCSGPLR 417 VHYVPWDQLFRNPHQALLHTANREPEDECVGEGLACHQLCARGHCWGPGFTQCVNCSGPLR 418	Qy 1003 TFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDP
POWALIN 186 334 CYS_RICH.	Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HASSP; PU1362; JECK.

R HASSP; PU1362; JECK.

R InterPro; JPR000194; EGFR L domain.

R InterPro; JPR000194; EGFR L domain.

R InterPro; JPR000174; Furin-like.

R InterPro; JPR001290; Ser_thr_pkinase.

R InterPro; JPR001290; Jryr_pkinase.

R InterPro; JPR001290; TYR_INASE.

R Ffam; PF00100; TYR_INASE.

R FAMT; PR00100; TYR_INASE.

R SMART; SM00261; FU; 5.

R SMART; SM00261; FV; 5.

R SMART; SM00219; TYRC; 1.

R SMART; SM00219; TYRC; 1.

R SMART; SM00219; TYRC; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

R PROSITE; PS50011; PROTEIN KINASE DOM; 1.

R Transmembrane; Glycoprotein; Receptor; Signal; Transferase; Transmembrane; ATP-binding; Phosphorylation; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                           Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine kinase precursor (EC 2.7.1.112)
                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomoropha, Acanthopterygii, Percomorpha, Atherinomorpha,
Cyptinodontiformes, Poeciliidae, Xiphophorus.
                                                                                                                                                                                           SEQUENCE FROM N.A.

MIRDLINES-80015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F.,
Telling A., Robertson S.M., Schartl M.;
Telling A., Robertson S.M., Schartl M.;
Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu locus in Xiphophorus.";
Nature 341:415-421(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MELANOMA RECEPTOR PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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EXTRACELLULAR (POTENTIAL)
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ATP (BY SIMILARITY).
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                                                                                  Kiphophorus maculatus (Southern platyfish).
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FID 237 245 BY SIMILARITY. FID 241 253 BY SIMILARITY. FID 269 296 BY SIMILARITY. FID 300 311 BY SIMILARITY. FID 303 313 BY SIMILARITY. FID 504 513 BY SIMILARITY. FID 508 521 BY SIMILARITY. FID 509 BY SIMILARITY. FID 517 BY SIMILARITY. FID 526 569 BY SIMILARITY. FID 518 SIMILARITY. FID 519 BY SIMILARITY. FID 520 615 BY SIMILARITY. FID 510 BY SIMILARITY. FID 511 BY SIMILARITY. FID 521 BY SIMILARITY. FID 522 634 BY SIMILARITY. FID 618 626 BY SIMILARITY. FID 618 GCCNAC) (POTENTIAL). FID 510 N-LINKED (GLCNAC) (POTENTIAL). FIN 511 411 HA N-LINKED (GLCNAC) (POTENTIAL). FIN 512 365 365 N-LINKED (GLCNAC) (POTENTIAL). FIN 513 516 S10 N-LINKED (GLCNAC) (POTENTIAL). FIN 514 517 HA N-LINKED (GLCNAC) (POTENTIAL). FIN 516 576 N-LINKED (GLCNAC) (POTENTIAL). FIN 517 576 S76 N-LINKED (GLCNAC) (POTENTIAL). FIN 518 518 N-LINKED (GLCNAC) (POTENTIAL). FIN 519 54 MY, 4793E0749DCIDSSA CRC64;	cch 38.9%; Score 2652.5; DB 1; Length 1167; al Similarity 44.8%; Pred. No. 8.6e-134; 569; Conservative 169; Mismatches 388; Indels 145; Gaps 31;	4 AALCRWGILLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 59	60 LELTYLPTNASLSFLØDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119 	120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL 179 	180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLIRTVCAGGC-ARCKGPLPTDCCHE 238 :	139 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298	299 CPYNYLSTDVGSCTLVCPLANQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358	S9 ITEL-EFAGCKKIFGSLAFLPESFDGDPASNTAPQYIKANSKFIGITELTGYLYISA 414	15 WPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTH 473	74 LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ 533	34 FLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDP 5 1	94 PFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS 65
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1133 CSPQPEYVNQPDVRPQP-----PSPRE-----GPLP-AARPAGATLERAKTLSPGKNG
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                                         645 AVGLVSGLLITVIVALLIVVLLRRRRIK-RKRTIRCLLQEKELVEPLTPSGQAPNQAFLR
                                                                              1LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM
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                             654 IVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMR
                                                                     714 ILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYV
                                                                                                           MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
                                                                                                                                                SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES
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Eukaryogici, Metacamini,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A., "Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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MEDLINE=90311312; PubMed=2164210;
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R InterPro; IPR00019; Euk pkinase.

R InterPro; IPR0001719; Euk pkinase.

InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R Pfam; PF00150; Recrp. L domain; 2.

R PRART; SM00261; Euk pkinase; 1.

R SMART; SM00219; Tyrc; 1.

R SMART; SM0019; PROTEIN KINASE ATP; FALSE NEG.

R ROSITE; PS00107; PROTEIN KINASE DOM; 1.

R ROSITE; PS00101; PROTEIN KINASE DOM; 1.

Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;

W Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

R SIGNAL

SIGNAL
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- LALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, ESTST DUE TO ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
-!- TOWN SHID DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SHID OF MAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SHID OF MAINS OF MAIN SIGNAL-TRANSDUCING PROTEINS.
-!- FTM: LIGAND-BINDING INCRASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE PRES SUBUNIT OF PHOSPHATIDYLINOSITOL 3 KINAGE (BY SIMILARITY).
-!- DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
                                   Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an additional epidermal growth
                                                                                                                                                                                                                                                                 MEDLINE=9328282; PubMed=7685162; Match M.; Match M.; Vazaki Y., Sugimura T., Terada M.; Match M.; Vazaki Y., Sugimura T., Terada M.; CerbB3 gene encodes secreted as well as transmembrane receptor tyrosine kinase..; Matchen Biochen. Blophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BIMDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
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CYTOPLASMIC (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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BY SIMILARITY.
                                                                                                  factor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
                                                                                                                                                                                                        SEQUENCE FROM N.A. (SHORT FORM).
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MIM; 190151; -.
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            DOLFRNPHQALLHTA - NR PEDECYGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECV
                                EECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
                                                                                                THCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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062799; 062955;
15-007-2002 (Rel. 37, Created)
15-007-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
(c-erbb3).
ERBB3.
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34.9%; Score 2375.5; DB 1; Length
Best Local Similarity 40.0%; Pred. No. 5.3e-119;
Matches 525; Conservative 197; Mismatches 457; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U29339; AAC28498 2; ...

R EMBL; U52530; AAC53050.1; ...

R HSSP; PI362; IFGK.

InterPro; IPR000494; EGFR L domain.

InterPro; IPR000179; Euk pkinase.

R InterPro; IPR001274; Furin-like.

R InterPro; IPR001274; Furin-like.

R InterPro; IPR001274; Furin-like.

R InterPro; IPR001274; Furin-like.

R Pfam; PF00757; Furin-like; 1.

R Pfam; PF00109; Furin-like; 1.

R Pfam; PF00109; TYRKINASE.

R PROBOTIS; PR00109; TYRKINASE.

R SWART; SM00219; TYRK; 1.

R SWART; SM00219; TYRK; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYR; 1.

R PROSITE; PS00101; PROTEIN_KINASE DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE DOM; 1.

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                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: THE CYTOPHASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCITATION WITH THE PRS SUBUNIT OF PHOSPHATIDYLINGSTOL STANDER.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                        SEQUENCE OF 922-1097 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Sciatic nerve;
MEDLINE-97184212; PubMed=9030624;
MEDLINE-97184121; PubMed=9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;
"Expression of neuregulins and their putative receptors, ErbB2 and
ErbB3, is induced during Wallerian degeneration.";
Brownesci. 17:1642-1659(1997).
I-FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
I-CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
STRAIN=Sprague-Dawley; TISSUE=Liver; MEDLINE=96096535; PubMed=8522190; Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.; Tellyng of the rat ErbB3 cDNA and characterization of the recombinant protein."; Gene 165:279-284(1995).
                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                            REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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19.40412; 054601; 09W2G0; P81868;
13.404-1987 (Rel. 05, Created)
15.DEC-1998 (Rel. 37, Last sequence update)
16.OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)
(Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB)
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Clifford R., Schupbach T.;
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides F.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
B. Amanatides F.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
B. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Fleelifer B.D.,
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RA Grerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A daria D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
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Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
Steince 287:2185-2195(2000).
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Several lavels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
Dev. Biol. 205:129-144 (1999).
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MEDLINE=85137938; PubMed=2983232;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal
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STRAIN-Oregon-R; TISSUE=Embryo;
MEDLINE=87002474; PubMed=3093080;
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                                                                                                                                MEDLINE-85124611; PubMed-2982499;
Livneh E., Glazer L., Segal D., Schlessinger J., Shilo B.-Z.
The Drosophila EGF receptor gene homolog: conservation of l
hormone binding and kinase domains.";
Cell 40:599-607(1985).
Clifford R., Schupbach T.;
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                                                                                                   SEQUENCE FROM N.A.; AND ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUNCTION BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A WINIAD OF DEVELOPMENTAL DECISIONS.
CRITICAL FOR THE PROLIFERATION OF INAGINAL TISSUES, AND FOR THE POLLERERATION OF INAGINAL TISSUES, AND FOR THE POLLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF ANNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BALIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGP RECEPTOR FAMILY.
                                                                                               SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                          Perrimon N., Perkins L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                                          ANALYSIS.
MEDLINE-92038942; PubMed-1936959;
Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF052754; AAC08536.1; -. EMBL; AF052753; AAC08536.1; JOINED. EMBL; AF052754; AAC08535.1; -. EMBL; AF052752; AAC08535.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97248481; PubMed=9094709;
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growth factor receptor.";
Nature 314:178-180(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF receptor.";
Cell 89:13-16(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITEL-----EFAGCKK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 IFGSLAFLPESFDG--DPASN--TAPQYIKANSK----FIGITELTGYLYISAWPDSLPD 421
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Receptor; Phosphorylation; Transferase; Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing; Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.2%; Score 1922; DB 1; Length 1426; Best Local Similarity 32.4%; Pred. No. 7.3e-95; Matches 464; Conservative 184; Mismatches 432; Indels 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPIDERMAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                          SMART; SM00261; FU; 7.
SMART; SM00219; TYrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS001109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PIR; A00640; GQFFE.
HSSP; P11362; 1FGK.
FlyBase; FBGN0003731; Egfr.
InterPro; IPR000494; EGFR L. domain.
InterPro; IPR001049; Euk Pkinase.
InterPro; IPR002104; PurIn-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Ffam; PF001030; Recep L. domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk pkinase; 1.
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1069
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                                                                                                                                                                                                                              603 JADCGYISNAYK--FDNRTCKICHPECR-----TCNGAGADHCQECVHVRDGQHCVSEC
                                                                                                                                                                                                                                                                                    SQMMLITQLMPLGCLLDYVRNNRDKIGSKALLNWSTQIAKGMSYLEEKRLVHRDLAARNV
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                                                                                                                       714 GY--FWEYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKRREQCET
                                                                                                                                                     -----SC----NDLDDKG-----SC----
                                                                                                                                                                              ECPADHYTDEEQRECFORHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNSTMFNCTS
                                                                                                                                                                                                             -CPAEQR----IVSAVVGILLVVVLGVVFGI
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Viruses, Retroid viruses, Retroviridae, Alpharetrovirus.
VCBI_TaxID=11864;
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15-JUM-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB
V-ERBB.
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15-JUL-1999 (Rel. 38, Last seq
15-JUN-2002 (Rel. 41, Last ann
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. The European Droinformatics Institute of the European of the Statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                             LYTOSINE PHOSPHATE.

MISCELLANBOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLBUKEMIA CELLS
IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE
C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

MISCELLANBOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                  ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R EMBL, M10066; AAA48763.1; ALT_INIT.
R PIR; A00643; TVCHLV.
R PIR; BOOG43; TVCHLV.
R HSSP; P11362; 1FGK.
R InterPro; IPR000719; Euk_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Prom; PF00069; pkinase; 1.
R PRINTS; PR00109; TYRKINASE.
R ProDom; P000001; Euk_pkinase; 1.
R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
R PROSITE; PS00109; PROTEIN KINASE DOM; 1.
R TRAINSFEASE; Tyrosine-protein kinase; ATP-binding; Oncogene; Glycoprotein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.3e-86;
); Mismatches 135; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 634;
SEQUENCE FROM N.A.
MEDLINES 8522822; PubMed=2988784;
Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
Crittenden L.B., Raines M.A., Kung H.-J.;
"c-exbB activation in ALV-induced erythroblastosis: novel
processing and promoter insertion result in expression of
amino-truncated BGF receptor.";
Cell 41:719-726 (1985).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E705E33A0BE01FCC CRC64;
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ATP (BY SIMILARITY)
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Matches 370; Conservative
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183 TVLDFASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCHNQ 242
                                                                                                                      CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC 299
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22.8%; Score 1553; DB 1; Length 703;
Best Local Similarity 43.9%; Pred. No. 1.4e-75;
Matches 311; Conservative 109; Mismatches 258; Indels 30; Gaps
                                        REMBL, M20386; AAA48760.1;
R InterPro; IPR000494; EGFR_L domain.
R InterPro; IPR000194; EGFR_L domain.
R InterPro; IPR0001245; Tyr_Dkinase.
R InterPro; IPR002174; Furin-like,
R Ffam; PF01030; Recep_L_domain, 2.
RAMAT; SM00261; FU; 4.
R PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.
R PROSITE; PS00109; PROTEIN KINASE ATP; PARTIAL.
R PROSITE; PS00101; PROTEIN KINASE DOM; PARTIAL.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
T SIGNAL.

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              email to license@isb-sib.ch)
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SEQÜENCE
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LTYLPTNASLSFLODIQEVOCYVLIAHNOVROVPLORLRIVRGTOLFEDNYALAVLDNGD 121

PLNNTTPVTGASPGGLRELQLRSITEILKGGVLIORNPQLCYODTILWKDIFHKNNQLAL 181

TLID-TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ 239

8 RWGLLLALLPPGAA----STOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLF 61

13 62

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July 22, 2003, 08:11:38; Search time 37.9774 Seconds (without alignments) 4403.399 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Pullall lleredulin 2	Human tyrosine kin	HER2 transcene nla	Himan HERO (Frhe)	HFD-2/new protein	Direct procession	no nair/2-van mampu	Human HER-2/neu pr	Amino acid semen	omers of the state	namer upwer by	HER2/neu amino aci
SOMMAKIES			ΩI	AAV92620	0707/150	AAE12130	AAB60167	AAU74545	AAWO1111	20 A C O W C C	0000000	AAB21198	AAY84780	AABAGAGA	000000000000000000000000000000000000000	AAG88267
			DB		1	22	22	23	17	2	2	77	21	22	1	22
			re Match Length DB I	1255	1	1255	1255	1255	1255	1255	1 (1722	1255	1255		1255
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Human Her-2 protei	Her-2/		Human Her-2/neu po	ice of c-er	Human breast cance	Human HER-2/neu pr	Rat HER-2/neu prot	Rat Her-2/neu onco	Mouse Her-2/neu pr	acid seque	Her-		Her-2/neu extracel	Mouse Her-2/neu ex	Mouse Her-2/neu ex	Human HER-2/neu fu	Her-2/neu extracel	Her2-GM-CSF immuno	Extracellular HER-	Human Her-2/neu on	Human ErbB2 oncopr	Erb82	DC8scFv-erbB2EC fu	Extracellular port	Amino acid sequenc	Human EGF receptor	Human Her-1 protei	epider	Amino acid sequenc	a]	ч	44	щ	44
AAE24067	AAE20479	AAM51143	AAU77114	AAR39568	AAU98923	AAB21208	AAB21199	AAM51144	AAB21206	AAG62860	AAM51151	AAB21203	AAM51148	AAM51152	AAM51153	AAB21204	AAM51149	AAW19764	AAB21200	AAM51145	AAB60408	AAB61593	AAY44993	AAR08222	AAB19259	AAY50616	AAE23019	AAM50768	AAB68420	9	AAE20483	AAE20481	à	AAE20482
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1255	1255	1255	1255	1433	1223	1200	1256	1256	1256	1256	1256	919	919	920	926	712	712	782	653	653	645	645	951	624	1210	1210	1210	1210	1210	1210	583	587	289	009
98.7	98.7	98.7	98.7	98.1	96.3	94.1	87.2	87.2	86.8	86.8	86.8	70.6	9.02	9.69	59.6	54.3	54.3	52.1	52.1	52.1	51.5	51.5	9.09	49.1	46.2	46.2	46.2	46.2	46.1	45.6	45.3	45.3	45.2	45.2
6728	6728	6728	6728	6685	36	급	941.	ä	914.	914.		ᆵ	4814	ŏ		3698	3698	3552	3550	3550	3512	3512	44	3344	3146	3146	3146	3146	3144	3105	3084	3084	3083	3083
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38			41	42		44	45

ALIGNMENTS

RESULT 1

AAY9 ID	AAY92620 ID AAY92620 stan	620 AAY92620 standard; Protein; 1255 AA.
AC	AAY92620;	
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DE	Human heregulin 2 (Her2).	in 2 (Her2).
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¥	Heregulin 2;	Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity:
X.	self-protein;	self-protein; cancer; breast cancer; prostate cancer;
X.	cell-associat	ed peptide antigen; foreign epitope.
×		
SO	Homo sapiens.	
×	1	
H	Key	Location/Qualifiers
	Domain	1173
		/label= N-terminal
답		/note= "mature polypeptide"
	Region	525
		/label= insertion region
		/note= "suitable for foreign epitope insertion"
	Region	5973
		/label= insertion region
		/note= "suitable For foreign epitope insertion"
F.	Region	103117
		/label= insertion region
		/note= "suitable for foreign epitope insertion"
	Region	149163
		/label= insertion_region
		/note= "suitable For foreign epitope insertion"
FI	Domain	174323

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This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and Cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T helper epitopes were identified (see features table). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate cancer
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|abel= ingertion_region
|note= "sultable For foreign epitope ingertion"
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|/label= insertion region
|note= "suitable for foreign epitope insertion"
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|Tabel= insertion region
|note= "suitable For foreign epitope insertion"
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/note= "suitable for foreign epitope insertion"
/label= C-terminal_domain
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1906== insertion region
/note= "suitable for foreign epitope insertion'
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/note= "suitable For foreign epitope insertion"
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'note= "suitable for foreign epitope insertion'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haaning J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                                                                                                                                                                                                                                                                                        55..1010
|abel= Tyrosine_kinase_domain
                                                                         324..483
/label= Ligand_binding_domain
                                                                                                                                                                          /label= insertion region
/note= "suitable for foreign
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|Tabel=_Cysteine_rich_domain
label Cysteine_rich_domain
                                                                                                                                                                                                                                                               label= Transmembrane_domain
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is used for inducing immune responses against weakly immunogenic cell-associated bettide antigens (PA) such as those associated with cencers (self-proteins).

Cancers (self-proteins).

(PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGR8b).

The method comprises effecting simultaneous presentation by antigen producing cells (APC8) of the animals immune system of: (1) at least 1 and (2) the animals immune system of: (3) at least 1 B-cell group derived from the PA and/or at least 1 b-cell group derived from the FGR8b comprising of human PSM, human Her2 and human-munime FGR8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
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YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFT
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                                                                                                                                                                                                                                     Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
                                                                                                                                                                                                                                                                                                                                                Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MHC; immunoregulatory; immune response; HER-2; adoptive immunotherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                                                                                                                                            GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
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774..782
/note= "Antigenic epitope"
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peptides) with enhanced binding to major histocompounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative co their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers controlled by expression of the breast cancer antigen, HER-2. Polymucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polymucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide
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                   The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. In particular, the antibody is directed against ErbB2 (also known as HER2 and p195neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
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is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytoned conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                           Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering anti-ErbB antibody-maytansinoid conjugate to the mammal
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(SCHW/) SCHWALL R.
(SLIW/) SLIWKOWSKI M.
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HER-2/neu oncogene i
                                                                                                                                                                                                                                                                                                                       HER-2/neu; c-erbBl; p185; oncogene; tyrosine protein kinase; breast cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
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Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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                                                                                                                                        MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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95US-0414417.
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17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
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                                                   IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                        EEYLVPQQGFFCPDPAPGAGGWHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
              HQSDVWSYGVIVWELMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKCWM
                                                                                                                                                               AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                          EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                                                                                                                                                                                                                                                                        HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                           GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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(SMIK ) SMITHKLINE BEECHAM.
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                                                                                                                                                                                                                                          The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; cell transformation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
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                                                                                             NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                        AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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Best Local Similarity 98.6%; Pred. No. 0;
Matches 1238; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                     Human HER-2/neu protein.
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Similarity

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The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytocoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I) bound to a culture in vitro and binds to a complex of an epitope (I) bound to a converse of the period of the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (II) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for inducing cellular immune response for the contigen when incubated with a T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope contined to antigen when incubated with a T lymphocyte to (I) or (II). Epitope CC antigen when incubated with a T lymphocyte to (I) or (II). Epitope CC antigen when incubated with a T lymphocyte to (I) or (II). Epitope CC enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine convides the ability to direct and focus an immune response to multiple tumour associated molecules addressing the problem of tumour cumultiple tumour associated molecules addressing the problem of tumour cumultiple tumour associated molecules addressing the problem of tumour cumultiple tumour associated molecules addressing the problem of tumour cumultiple tumour associated molecules addressing the problem of tumour cumultiple tumour associated molecules addressing the problem of tumour cumultiple tumour sariability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in experimental
NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
                                                                                                                                                                                                                                                                                                                                                                        Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
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cellular immune responses for the prevention and treatment of cancer
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                                                                           NOPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antisense oligonucleotide which modulates the expression of Hums
Epidermal Growth Factor receptor, Her2, is useful for treating tumors
inflammation or to prevent infection in humans -
EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
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                                                               NOPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                            GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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98.7%; Score 6728;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1238; Conservative 5; Mismatches
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N-PSDB; AAD38904.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukcoyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, preventions, e.g., vaccine and other compositions for the diagnosis, preventions and treatment of human malignancies, for stimulating the development of cancer in a complement. The invention is useful for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a comman patient, as probe or primer for nucleic acid hybridisation, to compensively form duplex molecules with complementary stretches of the centire Her-2/Neu gene or gene fragments of interest, to isolate a full centive Her-2/Neu gene or speciale host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immuncherapy of breast cancer and other Her-2/Neu-

Superpress associated malignancies. The invention is useful in gene therapy. The
1141 NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ 1200
                                                                                                                                                                                                                                                                                 Location/Qualifiers
1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
                                                                                                                                                                                                                          Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
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                                      GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV
                                                  Kalos MD;
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28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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Mcneill PD, Vedvick TS;
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EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of human Her-2/neu (p185 glycoprotein or c-etbb2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFK), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, inucleic acids encoding them, viral vectors, and vaccines
                                                                                        NQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                       AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                           NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQ
                                                                                                                                         GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                         AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
                                                                                                                            GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
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                                                                                                                                                                                                                                                                                           Human Her-2/neu oncogene-encoded p185 glycoprotein.
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comparising the fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain of protein is fused to a Her-2/neu intracellular domain of response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ax vivo with a nucleic acid cells to the animal. The fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu cusion protein can be used to remove tumour cells from a sample in corder to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Zheu or a polymucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
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                                                                                                                                                                                                                                                        HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                           IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                        EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGDLTLGLEPSEEAPRSPLAPSEG
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acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000; 2000US-0675904.
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                                                   VEECRVLQGLPREYVNASHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
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                           DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                  MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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- for imaging or treating breast
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2003, 08:22:34 ; Search time 48.3575 Seconds Run on:

(without alignments) 5347.444 Million cell updates/sec

Title: Perfect score:

SEQ4-325-339-12 6814 1 MELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1255

Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

671580 segs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
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SUMMARIES

099X70 rattus norv 099X98 mus musculu 09yH40 xiphophorus 09w6f6 gallus gall 09bf19 anopheles g 09uk79 homo sapien 08r2x1 mus musculu 08r712 avian rous-086712 avian rous-086714 avian rous-086714 avian reus-086714 avian eryth 08syv0 homo sapien 08syv0 mus musculu 09wyf5 mus musculu O18735 canis famil Description Q9QX70 Q9EP98 Q9YH40 Q9W6F6 P79754 Q9BIH9 Q9UK79 Q8R2X1 Q86712 Query Match Length DB 1210 1165 1137 1328 1433 Score Result Š.

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NQPDVRPQPPSPREGPLPAARPAGATLER-----AKTLSPGKNGVVKDVFAFGGAVENPE
                                   AGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYV
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STRAIN=FIGHER, TISSUE=LIVER;
MEDLINE=902588889 PubMed=2342466;
MEDLINE=902588889 PubMed=2342466;
Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.,
Earp H.S.;
"A truncated, secreted form of the epidermal growth factor receptor is encoded by an alternatively spliced transcript in normal rat tissue."
Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rat
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R InterPro; IPR000199; Euk Dkinase.
InterPro; IPR00114; Furin-like.
R InterPro; IPR001214; Furin-like.
R InterPro; IPR001205; Tyr Dkinase.
R Ffam; PP000757; Furin-like; 1.
R Pfam; PP00069; pkinase; 1.
R Pfam; PP001009; Recep L domain; 2.
R RNART; SM00109; TYRKINASE.
R SMART; SM00109; TYRKINASE DOM; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
R PROSITE; PS00109; PROTEIN KINASE TYR; 1.
R ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE 1209 AA; 134891 MW; 96FEB7F6CC1B7773 CRC64;
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STRAIN=FISHER; TISSUB=LIVER;
Guttridge K., Dawson T.L., Earp H.S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; M37334, ARF14008.1; -
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petch L.A.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 46.1%; Score 3144; DB 11; Local Similarity 50.3%; Pred. No. 3.1e-228; Nes 643; Conservative 165; Mismatches 354;
                                                                                                                                                                                                             1209
                                                                                                                                                                                                           PRT;
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SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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Best Local S:
Matches 643,
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91.2%; Score 6217; D
90.9%; Pred. No. 0;
ive 43; Mismatches
            Best Local Similarity 90.9
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                           PEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ------DE-----PERGAPPST
                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE; SEQUENCES STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schell C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubzamaniam S., Crossley T.O., Magnuson T.R., James C.D., Maihle N.J.;
                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoforms.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275364; AAG28045.1;
EMBL; AF275364; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; JOINED.
EMBL; AF275367; AAG24386.1; ---
HSSP; P11362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                 Epidermal growth factor receptor isoform 1. EGFR.
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PROSITE; PS00101; PROTEIN KINASE_DAW; 1.
PROSITE; PS50011; PROTEIN KINASE_DAW; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                  PRT; 1210
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InterPro; IPR000494; EGFR Li domain.
InterPro; IPR000494; EGFR Li domain.
InterPro; IPR002104; Eusi, Entrage.
InterPro; IPR002104; Furin-11ke.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Try Lipkinase.
Ffam; Pr00057; Furin-11ke; 1.
Pfam; Pr00059; pkinase; 1.
Pfam; Pr00069; pkinase; 1.
ProDom; PR00001; Euk_pkinase; 1.
SMART; SM00220; STKC; 1.
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                                                                                                            FKGTPTAENPEYLGLDVP 1254
                                                                                                                                                                                                  PRELIMINARY;
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STRAIN=C57BL/6J;
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                                    TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCA-RCKGPLPTDCCHEQ
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                                                                       PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1
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INTERPRO; IPR000494; EGFR L. domain.
INTERPRO; IPR000199; EUK_DKINASE.
INTERPRO; IPR001149; FUTIN-11ke.
INTERPRO; IPR001369; TURR_CG.
INTERPRO; IPR001369; TURR_CG.
INTERPRO; IPR001409; YLP_motif.
Pfam; PF000757; FUTIN-11ke; 1.
Pfam; PF001010; Recep L. domain; 1.
Pfam; PF001030; Recep L. domain; 1.
Pfam; PR010109; TYRKINASE.
PRODON; PD0000001; EUK_DKINASE.
PRODON; PD0000001; EUK_DKINASE.
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1141 NGMFLPAAENLEYLGL 1156
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SMART; SM00219; TYTKC; 1.
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Matches 534; (
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                                                                                                                                                                                                                                                                                                                                                                      CCHEOCAAGCTGPKHSDCLACLHFNHSG1CELHCPALVTYNTDTFESMPNPEGRYTFGAS
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                                                                                                                                                                                           56 VOGNIELTYLPTNASLSFLØDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA
                                                                                                                                                                                                                                                                                                                                              176 NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 KANSKFIGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYL
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                                  Query Match 40.0%; Score 2727; DB 13; Length 1165; Best Local Similarity 45.7%; Pred. No. 8.9e-197; Matches 583; Conservative 163; Mismatches 382; Indels 148;
  1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
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  SEQUEVCE
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                                    Query Match
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(010 EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
                                                                                                                                                                                                                                                                                                                                                                                                                    1176 GKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPS 1235
                                                                                                                                                                                                          1129 APLTCSPQPEYVNQPDVRPQP-----PSPRE----GPLP-AARPAGATLERAKTLSP
                                                                                                                                                                                                                                                                                                                           1070 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYV
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC
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MEDLINE=99263203; PubMed=10328884;
Dixon M., Lumsden A.;
Dixon M., Lumsden A.;
"Distribution of neuregulin-1 (nrgl) and erbB4 transcripts in embryonic chick hindbrain.";
MO1. Cell. Neurosci. 13:237-258(1999).
EMBL, AF121963; AAD31764.1; -.
HSSP; P11362; 1FGK.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor tyrosine kinase (Fragment).
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1055 KNNLPEKAKKAFDNPDYWNHSLPPRSTLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 LIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCA
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Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                 around the wntl locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1328 AA; 148613 MW; A333039258B647E9 CRC64;
                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
6rbB3.
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                                                                                                                                                                                                                                                                                                                               MEDLINE=99177347; PubMed=10077531; Gellner K., Brenner S.; analysis of 148 kb of genomic DNA around trubripes."; endines S.; analysis of 148 kb of genomic DNA around trubripes."; PRO56416; AAC34391.1; EMBL; AF056416; AAC34391.1; EMBL; AF056416; AAC34391.1; ENGO 11362; IFGK. InterPro; IPR000019; ENL pkinase. InterPro; IPR00019; ENL pkinase. InterPro; IPR00119; ENL pkinase. Feam; PF0075; Prini-like; IPFam; PF0075; Prini-like; IPFAMRT; SM00261; FUX. Jr. Prini-like; IPFAMRT; SM00261; FUX. Jr. Prini-like; IPFAMRT; SM00261; FUX. Jr. Prini-like; PS50011; PROTEIN KINASE DOM; IPFAMRT; PS00111; PROTEIN KINASE DOM; IPFAMRT; PROTEIN KINASE                                                                                               PRT; 1328
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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ESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCA
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                                                      AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF
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PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHT
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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37 140 104 199 164 257 223 282 377 329 429 449 FNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPL 317 85 9 QLRSLTEILKGGVLIQRNPQLCYQDTILWKDI-FHKNNQLALTLIDTNRSRACHPCSPMC 200 KGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLH 318 HNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELEFAGCKKIFGSLAFL 86 IAHNQVRQVPLQRLRIVRGTQLF-----EDNYALAVLDNGDPLNNTTPVTGASPGGLREL CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL GKMPQNSE-----CVPCKGVCPKTCPGEGI----VBDNIG----NYKDCTIIEGSLEIL 378 PESFDGDPASNT-----APLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQ 330 DQSFDGFQQVYTNFSFGPRYIKIDPDRLEVFSTVKEITGFINIQAHHPNFTTLNYFRNLE SDHEVWVQKNRNATECHEEGMECSEQCSKAGCWGKGPEQCLECKNVKYKGKCLDSCK---VIRGRILHNGAY-SLTLQGLGISWLGLRSLRSLGSGLALIHHNTHLCFVHTVPWDQLFRN PHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQ Gaps Length 1433; 385; Target Growth factor receptor.";

"Cloning, expression and localisation of the Anopheles gamb;
Epidarmal growth factor receptor.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

R HSSP; P11362; 1FGK.
R InterPro; IPR000145; CytC heme bind.
InterPro; IPR000145; CytC heme bind.
InterPro; IPR00019; Euk pkinase.
R InterPro; IPR0002174; Furin-like.
InterPro; IPR001245; Tyt pkinase.
R InterPro; IPR001245; Tyt pkinase.
R Pfam; PF00109; Pkinase; 1.
R Pfam; PF01030; Recept L domain; 2.
R Pfam; PF01030; Recept L domain; 2.
R SMART; SM00219; TYRKINASE.
R SMART; SM00219; TYRKINASE.
R SMART; SM00219; TYRC; 1.
R SMART; SM00219; TYRC; 1.
R PROSITE; PS00119; PROTEIN KINASE DOM; 1.
R PROSITE; PS00119; PROTEIN KINASE DOM; 1. Query Match

29.8%; Score 2029.5; DB 5; Length
Best Local Similarity 32.6%; Pred. No. 5.5e-144;
Matches 472; Conservative 197; Mismatches 393; Indels Receptor. 1 1 NON_TER 1 1 1 SEQUENCE 1433 AA; 159585 MW; E3D9D88967724F07 CRC64;

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241 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Doherry J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.D.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF177761, AAD56009.2; ...
InterPro; IPR000494; EGFR L. domain.
InterPro; IPR002174; Furin-Iike.
Pfam; PF01030; Recep L. domain; 1.
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OU-JUN-2002 (TERBLrel. 21, Created)
01-JUN-2002 (TERBLrel. 21, Last sequence update)
01-JUN-2002 (TERBLrel. 21, Last sequence update)
01-JUN-2002 (TERBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Hypothetical 40.2 kDa protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musl. TaxID=10090;
                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                              419 AA; 45472 MW; FECIBE347E2D030C CRC64;
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GLPREY - VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP
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           PQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMP1WKFPDEEGACQPCP1
                              Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Beug H.; Raynoscheck C., Jansson L., Doederlein G., Lhotak V., Johnsson A., Beug H.; Retroorviral capture of c-erbb proto-oncogene sequences: rapid evolution of distinct viral genomes carrying mutant v-erbb genes with different transforming capacities."; Oncogene 9:1307-1320(1994).

EMBL: $69372; AAC60727.1; -. HSSP: Pl1362; IFGK.

InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; I.
                                                                                NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTM
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
VCBI_TaxID=11950;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
V-erbB protein (Fragment).
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MEDLINE=94203659; Pubmed=8152791;
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RADINE=94203659; PubMed=8152791;

RA MEDLINE=94203659; PubMed=8152791;

RA Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,

RA Johnsson A., Beug H.; CerbB proto-oncogene sequences: rapid

RT "Retroviral capture of c-erbB proto-oncogene sequences: rapid

RT different transforming capacities.";

Concagene 9:1307-1320(1994).

RE EMBL, S69372; AAC60725.1;

RESP: P03322; LA6S.

DR HSSP: P03322; LA6S.

DR FIGHOROSTE: PROMOTOFS: Retro M.

InterPro; IPR001245; Tyr pkinase.

DR Fam, PF00269; pkinase; 1.

DR Pfam, PF002813; Retro M; 1.

DR ProDom; PD000001; Euk pkinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE PROTEIN KINASE SOURCE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE PROTEIN KINASE SOURCE; PS00109; PROTEIN KINAS
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                                                                                                  1 MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
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       Length 367;
                                        Indels
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Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
VCBI_TaxID=11950;
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Last annotation update)
   ; Score 1739; DB 11;
; Pred. No. 6.2e-123;
11; Mismatches 33;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
Query Match 25.5%
Best Local Similarity 88.0%
Matches 323; Conservative
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LGLDVPV 367
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01-NOV-1996
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POLYPROTEIN.
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Q64895;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gag, v-erb-A, v-erb-B protein.
Gag, V-ERB-A, V-ERB-B.
Avian erychroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
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MEDLINE=90206603; PubMed=1969616;
MEDLINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.Six amino acids from the retroviral gene gag greatly enhance th transforming potential of the oncogene v-erb-B.";
Oncogene 5:15-24(1990).
-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SIMILARITY: BELOMGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY:
EMBL, X52209; CAA36459.1; -..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.9%; Score 1697.5; DB 4; Length 412; Best Local Similarity 80.5%; Pred. No. 1e-119; Matches 330; Conservative 5; Mismatches 22; Indels 53;
Wan D.F., Gu J.R.;
"Novel human cDNA clones with function of inhibiting cancer of growth.";
growth.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF318349; AAL55856.1;
InterPro; IPR002049; EP-hand.
InterPro; IPR001219; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001019; VLP motif.
Pfam; PF00069; pkinase; I.
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412 AA; 44702 MW; 034397FF3F27D2BC CRC64;
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SMART; SM00219; TyrKc; 1.
PROSITE; PS000119; EF HAND; UNKNOWN 1.
PROSITE; PS500111; PROTEIN KINASE DOM; 1.
Hypothetical protein.
SEQUENCE 412 AA; 44702 MW; 034397FF31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG
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                                                                                                                                                                                                                                                                                                                                                                               ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
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Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                        Indels 102;
                                                                                                                                                                                                                                25.2%; Score 1718; DB 15; Length 567; 55.4%; Pred, No. 4.6e-121; ive 73; Mismatches 112; Indels 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAKTLSPGKNGVVKDVF------AFGGAVENPEYL 1197
                                                                                                                                                                          567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; E
Catarrhini; Hominidae;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 44.7 kDa protein.
PP3659.
Hymo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
SMART; SM00219; TYKK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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                                                                                                                                                                                                                                                              Best Local Similarity 55.49
Matches 357; Conservative
                                                                                                                 Tyrosine-protein kinase.
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SEQUENCE
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    R HSSP; P10828; ZNLL; CAASTASY 11; OLINED.

R INTERPRO; IPR000719; Euk_pkinase.

R InterPro; IPR000719; Euk_pkinase.

R InterPro; IPR001723; Stdhrm_receptor.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Ffam; PF00104; hormone_rec; 1.

R Pfam; PF00105; Zf-C4; 1.

R PRINTS; PR000401; Euk_pkinase; 1.

R PRINTS; PR000401; Euk_pkinase; 1.

R PRODOM; PD000001; Euk_pkinase; 1.

R PRODOM; PD000001; Euk_pkinase; 1.

R SWART; SW00219; TyrKc; 1.

SWART; SW00219; TyrKc; 1.

R PROSITE; PS00010; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R ATP-binding; DNA-binding; Nuclear_protein; Receptor;

R Transcription regulation; Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                        Ouery Match 24.3%; Score 1653.5; DB 15; Length 962; Best Local Similarity 51.7%; Pred. No. 7.4e-116; Matches 358; Conservative 73; Mismatches 142; Indels 119;
                                                                                                                                                                                                                                                                                                                  962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;
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CAA36459.1; JOINED
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RAY SEQUENCE FROM N.A.

REDIINE-88217326; PubMed=2897102;

RX MEDLINE-88217326; PubMed=2897102;

RX MEDLINE-88217326; PubMed=2897102;

RSOCTING P., Vennistrom B., Jansen M., Graf T., Beug H., Haymann M.J.;

RT "Common site of mutation in the erbB gene of avian erythroblestosis

RT "Common site of mutation in the erbB gene of avian erythroblestosis

RT virus mutants that are temperature sensitive for transformation.";

LO noogene RSE. 1.256-278(1987).

REMBL; X06943; CAA30024.1; -.

REMBL; X06943; CAA30024.1; -.

REMBL; ROSOUNG; PROTEIN KINASE.

REMBL; ROSOUNG; PROTEIN KINASE ATP; 1.

REMBL; ROSOUNG; PROTEIN KINASE DOM; 1.

REMBL; ROSOUNG; PROTEIN KINASE TYP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR
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                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis vitus (Ts34) v-erbB gene.
Viruses; Retroid viruses; Retroviridae; Avian type (NCBI_TAXID=11861;
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1197
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- LERAKTLS PGKNGVVKDVFAFGGAVENPEYL
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                                                                                    1111 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1169
                                                                                                               455 ------SRTPLLSSLSATSNNSATNCIDRNGG-------H-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=C3H/101, 129/SVJ, AND 129/SVFVTAC; Reiter J.L., Threadgill D.W., Eley G.D., Srrunk K.E., Danielsen A.J. Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maihle N.J.; "Alternative Transcripts from the Human and Mouse EGFR Genes Encode Carboxy-Terminal Truncated Receptors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor (Epidermal growth factor receptor isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative genomic sequence analysis and isolation of human and mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoforms.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        1170 AKTLSPGKNGVVKDVFAFGGAVENPEYL 1197
                                                                                                                                                                                                 Nature 409:685-690(2001).
EMBL; AF124513; AAD44149.1; -.
EMBL; AF2'5366; AAG28047.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 ASLSFLODIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 VTGASPGGLRELOLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - SHPSSCPKCDPSCPNGSCWGGGENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYOGCOVVOGNLELTYLPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 HFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAWPDNWTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVFONLOVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                           74 YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 -FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDL
                                                                                                                                                                                                                                                 1 22.1%; Score 1506.5; DB 11; Length 655; Similarity 44.5%; Pred. No. 5.2e-105; 35; Conservative 97; Mismatches 233; Indels 25;
                                                                                                                                                                                                           655 AA; 72906 MW; 6B34063B1BC928CB CRC64;
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                                                                             InterPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-Tike.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
EMBL, AKO04944; BAB23681.1; --
EMBL, AKO04983; BAB23641.1; --
EMBL, AKO04911; BAB23662.1; --
MQD; MQI:95294; Egfr.
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.5%
Matches 285; Conservative
                                                                                                                                                                    SMART; SM00261; FU; 3
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GenCore version 5.1.6
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- protein search, using sw model OM protein July 22, 2003, 08:12:49; Search time 10.2304 Seconds (without alignments) 5088.033 Million cell updates/sec Run on:

SEQ4-325-339-12
6814
1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1255 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P04626 homo sapien	P06494 rattus norv	Q60553 mesocricetu	P00533 homo sapien	_	Q15303 homo sapien		P13388 xiphophorus			P04412 drosophila				P13387 gallus gall		-	002466 branchiosto	Q9wtl4 mus musculu	P15127 rattus norv	P15208 mus musculu	_		9	_		P08069 homo sapien	Q60751 mus musculu	P24062 rattus norv	Q93105 aedes aegyp	80	SO homo sa	007494 gallus gall
SUMMARIES		ΩI	ERB2 HUMAN	ERB2_RAT	ERB2_MESAU	EGFR HUMAN	EGFR_MOUSE	ERB4 HUMAN	ERB4 RAT	XMRK_XIPMA	ERB3_HUMAN	ERB3 RAT	EGFR_DROME	ERBB ALV	ERBB_AVIER	ERBB_AVIEU	EGFR_CHICK	LT23_CAEEL	ERB2_MOUSE	ILPR_BRALA	IRR MOUSE	INSR_RAT	INSR_MOUSE	INSR_HUMAN	MIPR_LYMST	IRR HUMAN	IRR_CAVPO	HTK7_HYDAT	IG1R HUMAN	IG1R_MOUSE		INSR_AEDAE			EPB1 CHICK
		Match Length DB	1255 1	1257 1	1254 1	1210 1	1210 1	1308 1	1308 1	1167 1	1342 1	1339 1	1426 1	634 1	604 1	540 1	703 1	1323 1	245 1	1363 1	1300 1	1383 1	1372 1	1382 1	1607 1	1297 1	1300 1	1477 1	1367 1	1373 1	1370 1	1390 1	2146 1	987 1	984 1
	* Ouery	Match	98.7	87.1	86.9		45.8	43.5	43.2	39.4	35.6	34.5			25.0					10.7	10.3	10.2	10.2	10.2	10.2	10.1	10.1	10.1	9.4	9.1	9.1	9.1	•	8.9	8.8
		Score	6728	5937	5921.5	3144		2966.5	2947	2685.5	2423.5	2351.5	1952	1749.5	1703	1630	1595	1290	1142.5	727	669	969	695.5	695	693	069	685.5	685	641	623	619.5	618	615	605	599.5
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P09759 rattus norv Q03145 mus musculu	P54762 homo sapien Q91736 xenopus lae	P07949 homo sapien P54761 mus musculu	P29317 homo sapien 091571 xenopus lae	Q00944 gallus gall P53356 hydra atten	Q91738 xenopus lae P34152 mus musculu
EPB1_RAT EPA2_MOUSE	EPB1_HUMAN EPBB_XENLA	RET HUMAN EPB4 MOUSE	EPA2_HUMAN EPBA_XENLA	FAK1_CHICK HT16_HYDAT	FAK1_XENLA FAK1_MOUSE
984	984	1114	976	1053	1068
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596.5	590.5 588	588	584.5	573.5	569
34 35	36	38	0 4	4 4	4.4

ALIGNMENTS

PRESE HUMAN STANDARD; PRT; 1255 AA. P04626; 13.40C-1997 (Rel. 05. Created) 13.40C-1997 (Rel. 05. Last sequence update) 13.40C-1997 (Rel. 05. Last sequence update) 13.40C-1997 (Rel. 05. Last sequence update) 15.50N-2002 (Rel. 41. Last annotation update) 16.50N-2002 (Rel. 41. Last annotation update) 17. Toyoshima K.; 18.50N-2002 (Rel. 41. Last annotation update) 18.50N-2002 (Rel. 41. Last	ERBZ HUMMIN			
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    RESIDUES (BY SIMILARITY).
POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POLYMORPHISM: THERE ARE FOURS ALLELE BI (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
EXTRACELLULAR (POTENTIAL).
LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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EMBL, M11764, AAA35808.1, JOINED.
EMBL, M11766, AAA35808.1, JOINED.
EMBL, M11766, AAA35808.1, JOINED.
EMBL, M11730, AAA75493.1, -.
EMBL, M12036, AAA75493.1, -.
EMBL, X03363, CAA27060.1, -.
PIR, A25491, A25491.
HSSP, P11362, 1FGK.
Genew, HGNC:3430, ERBB2.
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YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLT 1198
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                                                                                                                                                                                                                                                                             PQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                               WMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV
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             SPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNMCVQIAKGMSYLED
                                                                        FTHOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
ERBB2 OR NEU.
Mesocriectus auratus (Golden hamster).
Mesocricetus Acazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
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SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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Best Local Similarity 87.0
Matches 1094; Conservative
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     RKVKVLGSGAFGTVYKGIWI PDGENVKI PVAIKVLRENTSPKANKEI LDEAYVMAGVGSP
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Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor ERBB2 OR NEU.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
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MEDLINE-92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,
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MEDLINE=91222560; PubMed=2025425;
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IN INTERPOS. IPROMO494; EGFR L. domain.
IN INTERPOS. IPROMO179; Euk pkīnase.
INTERPOS. IPROMO179; Euk pkīnase.
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Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
"Three dimensional structure of the transmembrane region of the proto-
oncogenic and oncogenic forms of the new protein.";
EMBO J. 11.43-48(1992).
-!- FUNCTION: ESSENTIAL. COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALDHA AND AMPHIREGULIN:
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
                                                                                                                                                                                                                                             THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER. SUBCELULIAR LOCATION: Type I membrane protein. PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY). SELONGS TO THE EGF RECEPTOR FAMILY.
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or send an email to license@isb-sib.ch)
                                                                   EMBL; D16295; BAA03801.1; -.
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HSSP; P11362; 1FGK.
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Maihle N.J.;
  NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGRNGVVKDVFAFGGAVENPEYLTPQ 1200
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MEDLINE=84219729; PubMed=6328312;
Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
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expression of the amplified gene in A431 epidermoid carcinoma cells.";
                                         GGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                   Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
                                                                                                    and
                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=97256547; PubMed=9103388;
MEDLINE=97256547; PubMed=9103388;

Takis J.V., Gariti J., Niederberger C., Scoccia B.;

"Expression of a truncated epidermal growth factor receptor-like protein (TEGFR) in ovarian cancer.";

Gynecol. Oncol. 65:36-41(1997).
                                                                                                                                                                                                                                                                                                                                                                                              Ilekis J.V., Stark B.C., Scoccia B.;
"Possible role of variant RNA transcripts in the regulation of
epidermal growth factor receptor expression in human placenta.";
Mol. Reprod. Dev. 41:149-156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reiter J.L., Maihle N.J.; "A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor."; Nucleic Acids Res. 24:4050-4056 (1996).
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SEQUENCE OF 575-687 FROM N.A.
Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
Lampland A.L., Balagubramaniam S., Crossley T.O., Magnuson T.R.,
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TISSUE=Placenta;
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MEDLINE=97078686; PubMed=8918811;
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MEDLINE=95382957; PubMed=7654368;
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MEDLINE=85270438; PubMed=2991899;
Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
"Characterization and sequence of the promoter region of the human
epidermal growth factor receptor gene.";
Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
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Biochem. Biophys. Res. Commun. 124:125-132(1984).
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Roe B.A., Merlino G.T., Pastan I.;
"Human epidermal growth factor receptor cDNA is homologous to
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MEDLINE=86046483; PubMed=6093780;
Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter O'Malley B.W.;
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Haley J.D., Waterfield M.D.;
"Contributory effects of de novo transcription and premature transcript termination in the regulation of human epidermal factor receptor proto-oncogene RNA synthesis.";
J. Biol. Chem. 266:1746-1753(1991).
'Human and mouse alternative EGFR transcripts encoding only
                                      extracellular domain of the receptor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                    SEQUENCE OF 713-924 FROM N.A. MEDLINE=84196372; PubMed=6326261;
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MEDLINE=84191554; PubMed=6325948;
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Nature 309:270-273(1984).
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98225196; PubMed=9556602; Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.; Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.; "Disulfide bond structure of human epidermal growth factor receptor."; J. Biol. Chem. 273:11150-11157(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/tuncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                      atypical
                                                                          domain
                ASN-528.

MEDLINE=96198132; PubMed=8962717;
Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
"Analysis of the glycosylation patterns of the extracellular domai
the epidermal growth factor receptor expressed in Chinese hamster
ovary fibroblasts.";
Growth Factors 13:121-132(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p60/
truncated isoform/TEGFR, 3/p110 and 4; are produced by
alternative splicing.
TISSUE SPECIFICTTY: Expressed in placenta. Isoform 2 is also
expressed in ovarian cancers.
MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of cell
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
  AND
                                                                                                                                                                                   ASN-633.
MEDLINE=20198209; PubMed=10731668;
Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.;
"Characterization of the N-oligosaccharides attached to the atyr
Asn-X-Cys sequence of recombinant human epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
ASN-175; ASN-413; ASN-444
                                                                                                                                                                     SITES ASN-56; ASN-352; ASN-361; ASN-568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carpenter G.;
"Receptors for epidermal growth factor
                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. 56:881-914(1987)
CARBCHYDRATE-LINKAGE SITES ASN-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87297456; PubMed=3039909;
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AAC50796.1; -.
AAC50797.1; -.
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Indels 108;

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LLLALLPPGAA - - STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN

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Q------PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGS-TA 1192
1141 NQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TP 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C3H;
Eisinger D.P., Serrero G.;
Eisinger D.P., Serrero G.;
Submitted (UUT-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIR=BALB/C, and CD-1; TISSUE=Liver, and Decidua;
STRAIR=BALB/C, and CD-1; TISSUE=Liver, and Decidua;
MEDLINE=93126380; PubMed=76788348;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
in mouse blastcorysts during delayed implantation.";
proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                            -----DP-----PERGAPPSTFKGTPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=B6/C3; TISSUE=Liver; MEDLINE=94170986; PubMed=812525; Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S., Jenkins N.A., Lee D.C.; The mouse waved-2 phenotype results from a point mutation in the EGF receptor tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B., "Comparison of EGF receptor sequences as a guide to study the ligand
                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
Avoid A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor 2 (bek/KGFR) gene.";
                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                            QGGAAPQPHPPPAFSPAFDNLYYWDQ-
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MEDLINE=91232866; PubMed=2030916;
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STRAIN=BALB/c; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                    (bek/KGFR) gene.";
Oncogene 7:1957-1962(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes Dev. 8:399-413(1994).
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Q01279;
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tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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R InterPro; IPR000494; Egfr. L domain.

R InterPro; IPR000194; Egfr. L domain.

R InterPro; IPR0012174; Furin-like.

R InterPro; IPR001245; Tyr_pkinase.

R Ffam; PF00169; pkinase; 1.

R Pfam; PF00169; pkinase; 1.

R Pfam; PF00100; Recep. L domain; 2.

R Pfam; PF00100; Euk_pkinase; 1.

R SMART; SM00219; Tyrkc; 1.

R PROSITE; PS00100; PROTEIN KINASE ATP; 1.

R PROSITE; PS00100; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R Transmembrane; Glycoprotein; Receptor; Signal; Transferase; 1.

Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG 1080
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1092 YVNQ-SVPKRPAGSVQNPVYHNQPLHP-----APGRDLHYQN--PHSNAVGNPEYLN
                                                                                                                      DSECRPRFRELVSEPSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDA
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MEDLINE=91189574; PubMed=81831326;
Plowman G.D., Calouscou J.-M., Whitney G.S., Green J.M., Carlton G.W.,
Foy L., Neubauer M.G., Shoyab M.;
Tigand-specific activation of HRR4/pl80erb84, a fourth member of the
epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                            896 QSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMIMVKCWMI
                                                                                                                                                                                                                                                                                                                                                                   VSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRL
                                                                                                         VHRDLAARNVLVKSPNHVKI TDFGLARLLDI DETEYHADGGKVPI KWMALESI LRRRFTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UNC-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
(pl80erbB4) (Tyrosine kinase-type cell surface receptor HER4).
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Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
Klagsbrun M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue distribution and differential processing in response phorbol ester."; J. Biol. Chem. 272:26761-2678(1997).
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R InterPro; IPR00019; Euk DkInase.
R InterPro; IPR0002174; Purin-like.
R InterPro; IPR001274; Purin-like.
R InterPro; IPR00145; YuP_motif.
R InterPro; IPR00149; YuP_motif.
R Fam; PF00169; Pkinase.
R Pfam; PF00169; Pkinase.
R Pfam; PF00179; Purin-like; 1.
R Pfam; PF00179; YuP; 2.
R Prodom; P0000001; Euk_Dkinase; 1.
R Prodom; P00179; Proferin KINASE ATP; 1.
R PROSITE; PS00109; PROTEIN_KINASE ATP; 1.
R PROSITE; PS00109; PROTEIN_KINASE DOM; 1.
R PROSITE; PS00109; PROTEIN_KINASE; DOM; 1.
              2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTRACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF. TGF-A, AND AMPHIREGULIN. CATIVATE ACTIVITY: ATP + a protein tyrosine = ADP + protein
FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
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SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF THE OTHER ERBB
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HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERBB4.
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Best Local Similarity 45.2%; Pred. No. 3.1e-150;
Matches 609; Conservative 184; Mismatches 380;
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CNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGPGPDNCTKCSHFKDGPNCVEKCPD 595
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                         GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC-------PAEQRASPL
                                                                           TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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AC 062956; 0922N7;
TS-DEC-1998 (Rel. 37, Created)
DT 15-UNN-2002 (Rel. 41, Last sequence update)
DT 15-UNN-2002 (Rel. 41, Last annocation update)
DE Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
GN ERBB4 OR TYRO-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIŠSUE=Heart;
MEDLINE=98221155; PubMed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R.R., Opel D.J., Han X.,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley, TISSEN-Spinal cord;
MEDLINE=97184212; PubMed=9030614;
MEDLINE=97184212; PubMed=9030614;
MEDLINE=97184212; PubMed=9030614;
Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
IN-BURDING BEFLIKE GROWTH PACTOR, BEFACELLUIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF. TGF-A, AND AMPHIREGULIN (BY SIMILARITY).
--- CATIVATED ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphare.
-- SUBMUNT: HOWDINER OR HETERODIMER WITH EACH OF THE OTHER ERBE RECEPTORS (POTENTIAL).
-- SUBCELLULAR LOCATION: Type I membrane protein.
-- TISSUB SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE RELICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINASE ERBB-4.
                                                                                                                               TISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
Lai C., Lemke G.;
"An extended family of protein-tyrosine kinase genes differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00261; FU; 4.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; GlycoproteIn; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
              "Neuregulins promote survival and growth of cardiac myocytes.
Persistence of ErbB2 and ErbB4 expression in neonatal and adult
ventricular myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE . RESIDUES (BY SIMILARITY).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                               expressed in the vertebrate nervous system.";
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                                                                          Biol. Chem. 273:10261-10269(1998)
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InterPro; 1PR000719; Euk pkInase.
InterPro; 1PR00174; Furin-like.
InterPro; 1PR001245; Tyr pkinase.
InterPro; 1PR001245; Tyr pkinase.
InterPro; 1PR004019; YLP motif.
Pfam; PF00757; Purin-like; 1.
Pfam; PF001030; Recep L domain; 2.
Pfam; PF001030; Recep L domain; 2.
Pfam; PF00109; TYRKINASE.
PRODOM; PP000001; Euk pkinase; 1.
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                                                                                                               SEQUENCE OF 848-901 FROM N.A.
Marchionni M.A., Kelly R.A.;
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Qy 357 IGITELEFACCKKIFCGLAFLPESFDGAPANIAPLOPEGLOVFETLEBITGTLVISAMP 416 Db 349 DSSNIDKFINCTKINGNLIFLYGGAPANIADAIDPEKLANVFRTVRBITGFLAIGTWP 408 QY 417 DSLPDLSVFQNLQVIRGRILHNGAYSLTLGGLGISHLGLRSLRSGLALIHHNTHLCF 416 Db 409 PNATDFSVFSNLVTGARALLHTANREGELGGLACHGLARGANYTTDBSNLCY 468 QY 477 VHTVPWDQLFRNPHQALLHTANREEDECVGEGLACHGLCARGHCWGFGFTQCWCSGFLR 536 Db 469 YHTINMTLESTVWGRILYIRDNRARENCTAEGRACKHLCSNDGCWGFGPDQCWCSGFRS 526 Cy 477 VHTVPWDQLFRNPHQALLHTANREEDECVGEGLACHGLCARGHCWGFGPDQCWACAHKGDFF 536 Db 469 YHTINMTLESTVWGRILYIRDNRARENCTAEGRACKHLCSNDGCWGFGPDQCWACAHKGDFF 536 Ch 1 1 1 1 1 1 1 1 1 1	
DOMAIN 186 334 CYS-RICH.	576 N - LINKED 520 N - LINKED 520 N - LINKED 1062 S - > N (1) 1062 S - > N (2) 1062 S - > N (3) 1062 S - > N (4) 1064 S - > S S - > S - > S S - S - S S - S - S - S S - S -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMEL, X16891; CAA34770.2; -.

BR HSSP; P11362; 1FGK.

HSSP; P11362; 1FGK.

RILEEPRO; 1PR000794; EGFR L domain.

RILEEPRO; 1PR000719; Euk pkinase.

BR InterPro; 1PR00124; Tyr_pkinase.

BR InterPro; 1PR00129; Prinase; 1.

BR RINTS; PR00109; TYRKINASE.

BR RINTS; PR00109; TYRKINASE.

BR SMART; SM00219; TyrKc; 1.

BR SMART; SM00219; TyrKc; 1.

BR SMART; SM00219; PR0TEIN KINASE Tyr; 1.

BR PROSITE; PS001109; PR0TEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                        KINASE ACTIVITY
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma receptor protein-tyrosine Kinase precursor (EC 2.7.1.112)
XMRK OR TU.
                                                                  Xiphophorus maculatus (Southern platyfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopherygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                            Wittbrodt J., Adam D., Malitschek B., Maueler W., Raulf F., Telling A., Robertson S.M., Schartl M.; Movel putative receptor tyrosine kinase encoded by the melanomainducing Tu locus in Xiphophorus.";
                                                                                                                                                                                                                                                                                            Schartl M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
SUBMITTED FROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.
STALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                   tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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PROTEIN KINASE.
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AVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILK
                                     648 LVSGLLITVIVALLITVVLLRRRRIK-RKRTIRCLLQEKELVEPLTPSGQAPNQAFLRILK
                                                              ETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1991 (Rel. 18, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB1) (Tyrosine kinase-type cell surface receptor HER3).
ERBB3 OR HER3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90083234; PubMed=2687875; Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A.; Isolation and characterization of ERBB3, a third member of the ERBB/epiderang growth factor receptor family: evidence for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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MEDLINE=90311312; PubMed=2164210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLILAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT FORM).

-i Alternative products: Two Forms, a long transmembrane form and a short secreted form, exist due to alternative Splicing.

-i Tissue specificity: Epithelial tissues and brain.

-i Tissue specificity: Epithelial tissues and brain.

-i- Damain: The Cytoplaramic Part of the Receptor may interact with the SH2 OR SH3 DOWAINS of WANY SIGNAL-TRANSDUCING PROTEINS.

-i- PTM: Ligand-Binding increases Phosphorylation on Tyrosine residues and promofes its Association with the PBS Subunit of PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).

-i- DISEASE: OVEREXRRESSED IN A SUBSET OF HUMAN MAWMARY TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000494; EGFR L domain.

R InterPro; IPR000199; EUK pKinase.

R InterPro; IPR0002174; Furin-like.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00059; pkinase; 1.

R Pfam; PF00050; Purin-like; 1.

R Pfam; PF0010001; EuK_pkinase; 1.

R Probom; P0000001; EuK_pkinase; 1.

R RART; SM00219; Tyrkc; 1.

R RART; SM00219; Tyrkc; 1.

R RART; SM00219; PROTEIN KINASE ATP; FALSE NEG.

R PROSITE; PS00110; PROTEIN KINASE_DOM; 1.

R PROSITE; PS50011; PROTEIN MINASE_DOM; 1.

Transferase; Tyrosine-protein; Multigene family; Receptor; Signal; Multigene family; Multig
Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L., Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an additional epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine Kinase.";
Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
MEDLINE=93282822; PubMed=7685162;
Katoh M., Yazaki Y., Sugimura T., Terada M.;
"c-erbB3 gene encodes secreted as well as transmembrane receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                       factor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (SHORT FORM).
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EMBL; M43409; AAA35799.1; --
EMBL; S61953; AAB26935.1; --
PIR; A36223; A36223.
HSSP; P11362; IFGK.
Genew; HGNC:3431; ERBB3.
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MIM, 190151;
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                              EECRVLOGLPREYVNARHCLPCHPECOPONGSVTCFGPEADOCVACAHYKDPPFCVARCP
                                                                                           THCNFLNGEPREFAHEAECFSCHPECQPMEGTATCNGSGSDTCAQCAHFRDGPHCVSSCP
                                                                                                                                         SGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRA----SPLTSIVSA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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es 452;
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R HSSP; PI1362; IFCK.
R InterPro; 1PR000494; EGFR L domain.
R InterPro; 1PR000419; Euk_pkinase.
R InterPro; 1PR001214; Furin-like.
R InterPro; 1PR001214; Furin-like.
R InterPro; 1PR001214; Furin-like.
R Pfam; PF00109; Furin-like; 1.
R Pfam; PR00109; Furin-like; 1.
R Pfam; PR00109; TYRKINASE.
R RNART; SM00201; FU, Euk_pkinase; 1.
R RNART; SM00201; FU, Euk_pkinase; 1.
R SMART; SM0109; PROTEIN KINASE TYP; 1.
R RNSITE; PS00107; PROTEIN KINASE TYP; 1.
R RNSITE; PS0011; PROTEIN KINASE DOM; 1.
R PROSITE; PS0011; PROTEIN KINASE DOM; 1.
R TRANBERASE; PS0011; PROTEIN KINASE DOM; 1.
R TRANBERASE; TYPOSINE, MULLigene family; Receptor; Signal; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
-:- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES
AND PROMOTES ITS ASSOCIATION WITH THE PBS SUBUNIT OF
PHOSPHATIDYLINOSITICL 3-KINASE.
-:- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=96096515; PubMed=8522190;
Hellyer N.J., Kim H.-H., Greaves C.H., Sierke S.L., Koland J.G.
"Cloning of the rat ErbB3 cDNA and characterization of the recombinant protein.";
                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                     REVISIONS TO 85; 513 AND 565.
Hellyer N.J., Koland J.G.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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584 HCVNSCPHGILG -- AKGPIYKYPDAQNECRPCHENCTQGCNGPELQDCLGQAEVLMSKPH 641
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                                                                                    SIVSAVVGILLVVVLGVVFGILIKRRQQKIR-KYTMRRLLQETELVEPLTPSGAMPNQAQ
                                                                                                                                                                                                        MRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEA
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FO4412; 061601; Q9W3C0; P81868;
13-AUG-1997 (Rel. 05, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Bard M. M. H.J., Zandell M.D., Zhang Q., Chen L.X., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Badakin D., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baladwin D., RA Beson K.Y. Banos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P., Andrews D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Botchan M.R., Dodgon K., Cawley S., Dallke C., Davenport L.B., Davies P., Andrews M., Cabriellan A.E., Gary N.S., Gelbart W.M., Glasser K., Robelt C., Gabriellan A.E., Gary N.S., Gabart W.M., Glasser K., Rodgon K., Doup L.E., Downes M., Dugan-Rocha S., Pleiter S.M., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Alalai M., Kalush P., Rapen G.H., Ke Z., Kunison J.A., Kerchum K.A., Alalai M., Kalush P., Rapen G.H., Ke Z., Kunison J.A., Kerchum K.A., Alalai M., Kalush P., Rapen G.H., Ke Z., Kunison J.A., Kerchum K.A., Alani M., Kalush P., Morntosh T.C., McLeod M.P., Mory W. Murphy B., Murphy L., Murry D.M., Nelson D.L., Mako P., Lei Y., Leitytek A.A., Liu X., Mattei B., McIntosh T.C., McLeod M.P., Pari V., Mory M. Murphy B., Murphy L., Murry D.M., Nelson D.K., Rames D. R., Mount S.M., Nixon K., Nixon R., Supski M., Roddage T., Keniscon M., Stupski M.P., Spier E., Spradling A.C., Siden-Kamos I., Simpson M., Stupski M.P., Wassarman D.A., Weisherock M., Wang D.A., Woodage T., Worley K.C., Wu D., Yang S., Zhon M., Zhong K., Nixon K., Zhong K., Zhon W., Zhong K., Zhong K., Zhon S., Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                           SEQUENCE FROM N.A., CHARACTERIZATI
STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE-87002474; Pubmed=3093080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF receptor.;

Cell 89:13-16(1997).

-:- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.

CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATE SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III, ARE PRODUCED BY ALTERNATIVE SPLICING.
TYPE III, ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERROR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX AND THORACIC AND ABDOMINAL GANGLIA.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                SEQUENCE OF 1133-1137; 1155-1167 AND 1209-1216 FROM N.A., AND MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perrimon N., Perkins L.A.; "There must be 50 ways to rule the signal: the case of the Drosophila
                                                                                                                                                                                                                                                        Raz E., Schejter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for
the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
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SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
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EMBL, AF052754; AAC08536.1; --
EMBL, AF052754; AAC08536.1; --
EMBL, AF052754; AAC08535.1; --
EMBL, AF052752; AAC08535.1; --
EMBL, K03416; AAA51462.1; --
EMBL, K03416; AAA51460.1; --
EMBL, K03416; AAA50965.1; --
EMBL, AF109077; AAD56132.1; --
EMBL, AF109077; AAD56132.1; --
EMBL, AF109077; AAD56132.1; --
EMBL, AF109078; AAD56132.1; --
EMBL, AF109078; AAD56132.1; --
EMBL, AF109078; AAD56133.1; --
EMBL, AF109078; AAD56133.1; --
EMBL, AF109081; AAD26130.1; --
EMBL, AF109083; AAD26131.1; JOINED.
EMBL, AF109083; AAD26131.1; --
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REVIEW
MEDLINE=97248481, PubMed=9094709;
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MEDLINE=92038942; PubMed=1936959; AFDLINE=92038942; PubMed=1936959; 
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    growth factor receptor."; Nature 314:178-180(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 KNFFDEAVSKEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACVRSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transmembrane; Glycoprotein; Receptor; Phosphorylation; Transferase; Tyrosine-protein kinase; ATP-binding; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.7%; Pred. No. 2.5e-96; nes 468; Conservative 183; Mismatches 429; Indels 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1952; DB 1; Length 1426;
Pred. No. 2.5e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPIDERMAL GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL) POTENTIAL.
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ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                        HASP, FILLOT, ALGON.

HASP, FILLOT, ALGON.

INTERPRO, IPRO00193; BGFR L domain.

INTERPRO, IPR000119; Buk PATNASE.

INTERPRO, IPR000114; Furin like.

INTERPRO, IPR001245; Tyr pkinase.

Fam, PF00055; Pkinase.

Fam, PF001030; Recep L domain; 2.

PFam, PF01030; Recep L domain; 2.

PRINTS; PR00109; TYRKINASE.

PRINTS; PR00109; TYRKINASE.

SWART; SW00261; FU; 7.

SWART; SW00261; FU; 7.
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X78919; CAA55522.1;
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890 YICRQKQKAKKETVKMTMALSGCEDSEPLRPSNIGANLCKLRIVKDAELRKGGVLGMGAP
                                                                                                                                                                                                                                                                                                                                                                   LVSEFSRMARDPQRFVVIQNEDLG--PASPLDSTFYRSLLEDD----DMGDLVDAEEYLVP
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                                                             PKNKYNDRGVCRECHATCDGCTGPKDTIGIGACTTCNLAIINNDATVKRCLLKDDKCPD-
                                                                                                         714 GY--FWEYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHBQVCSKCTHYKRREQCET
                                                                                                                                                                                               -ASPLTS------IVSAVVGILLVVVLGVVFGI
                                                                                                                                                                                                                                               LIKRRQQKIRKYT---MRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAF
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                                                                                                                                            ------ADPDDKG-----SC-----
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
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NCBI_TaxID=11864;
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                                                                                          SYMPIWKF -- PDEEGACQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQOKIRKYTWRRLLQETELVEPLTPSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        706 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                                    -i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-i- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS.
IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
-i- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             766 EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123; Gaps
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                                                                    RNA
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ProDom; PD000001; Euk_pkinase; 1.
SWART; SW00101; TYRKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
                               Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M., Crittenden L.B., Raines M.A., Kung H.-J.; "c-erbB activation in ALV-induced erythroblastosis: novel processing and promoter insertion result in expression of amino-truncated EGF receptor."; Cell 41:719-726(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.7%; Score 1749.5; DB 1; Length 52.3%; Pred. No. 5.7e-86; ive 79; Mismatches 135; Indels
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                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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ATP (BY SIMILARITY)
BY SIMILARITY.
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PIR; A00643; TVCHLV.
PIR; B00643; TVFVLV.
                  MEDLINE=85228222; PubMed=2988784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11362; 1FGK.
InterPro; 1PR000719; Buk pkinase.
InterPro; 1PR001245; Tyr pkinase.
Pfam; PP00069; pkinase; 1.
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Best Local Similarity 52.3
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
DOMAIN 13
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ACT SITE
SEQUENCE
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886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGVVKDVF------AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYY 1222
                                                                        ICTIDUYMIMUKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF 1004
                                                                                                                                                                  YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE 1064
                                                                                                                                                                                                                                                                                                                                                              1120 LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1177
                                                                                                 496 FLEESIDDGFL-----TAMVQ--LMPKKPS------TAMVQ 526
298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP 357
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DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS IN CHICKENS.

MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE
                                                                                                                                                                                                                                                                 PSEEEAPRSPL - - - - APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.;
                                                                                                                                                                                              MEDLINE-84026539; PubMed-6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima
"The erbB gene of avian erythroblastosis virus is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-152 FROM N.A.

MEDLINE=84223957; PubMed=6528658;
Debuire B., Henry C., Benaissa M., Biserte G., Claverie J.-M.,
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian erythroblastosis virus reveals
science 224:1456-1459(1984).
-!-CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
VCBI_TaxID=79685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDQ-----DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR FOR EPIDERMAL GROWTH FACTOR. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein erbB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 AA
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P00535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647 RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   76; Mismatches 128; Indels 126;
                                                                                                                             SMART; SM00219; TYKK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TRR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-profein kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                 Length 604;
                                                                                                                                                                                                                                                                                                                                                  76EBCDD06745D609 CRC64;
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ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

R -> W (IN REF. 2).

S -> F (IN REF. 2).

I -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.6e-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLYYWDQDPPERGAPPSTFKGTPTAENPEY 1248
                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 1703; 52.2%; Pred. No. 1.
EMBL; KO2006; AAA42394.1; ALT_INIT.
EMBL; KO1216; AAA42400.1; -.
PIR; AO0644; TVYUH.
                                              HSSP; P11362; 1FGK.
InterPro; 1PR000719; Euk pkinase.
InterPro; 1PR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
                                                                                                                                                                                                                   Phosphorylation
                                                                                                                                                                                                                                                                                                                                                    67633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.21
Matches 360, Conservative
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604 AA;
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DOMAIN 13
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CONFLICT
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                                                                                                                                                                                                                  EILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 IKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLEKGERLPQPP
                                                                                                                                                                                            ICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQ-NEDLGPASPLDSTF
                                                                                                                                                                                                                                                                                                                                                 1065 PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PVREDGFL-----PAPEYVNQ--LMPKKPSTAMVQNQIYNYISLTAISKLPIDSRYQN
                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                      CMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP
                                                                                                                 886 IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112) (CER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, anduction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                             703 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE=88261272; PubMed=3260329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1179 GVVKDVFAFGGAVENPEYL 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SHSTAVDNPEYL 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                             MEDLINE=87064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile
phenotype to ts167 avian erythroblastosis virus-transformed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                                                                                                                                                                                                                    Viruses, Retroid viruses, Retroviridae, Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 6:1751-1759(1986).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                          Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112) V-ERBB.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
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55.1%; Pred. No. 1e-79;
ive 69; Mismatches 119; Indels
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ATP (BY SIMILARITY)
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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InterPro; IPR000719; Buk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; P0000001; Euk pkinase; 1.
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Best Local Similarity 44.6%; Pred. No. 1e-77;
Matches 316; Conservative 111; Mismatches 251; Indels 30; Gaps
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                                                                                        SMART; SM00261; FU; 4.—
PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.
PROSITE; PS00109; PROTEIN KINASE TYR; PARTIAL.
PROSITE; PS50011; PROTEIN KINASE DOM; PARTIAL.
Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
TYrosine-protein Kinase; ATP-binding; Phosphorylation.
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                EMBL, M20386; AAA48760.1; -. Omain. InterPro: IPR000494; EGFR L domain. InterPro: IPR000494; Euk PArinase. InterPro: IPR00174; Furin-like. IrterPro: IPR001245; Tyr_pkinase. Pfam; PP00175; Furin-like; 1. Pfam; PP01009; Recep L domain; 2. SMART; SM00261; FU; 4.
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                                 TVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQ
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                    CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTPESMPNPEGRYTFGASCVTAC
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Job time : 20.2304 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human heredulin	Human tyroning kin	HER2 transcene nla	HIMMAN HERO	HER-2/nell protein	Himan HED-2/noil on	Human HFP-2/neu on	Amino acid sement	Himan HFD-2/neii	HER2/neu amino aci
SUMMARIES	AAY92620	AAE12130	AAB60167	AAU74545	AAW01111	AAW92406	AAB21198	AAY84780	AAB85458	AAG88267
08	21	22	22	23	17	20	21	21	22	22
% Query e Match Length DB	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
% Query Match	98.1	98.1	98.1	98.1	98.0	98.0	98.0	98.0	98.0	98.0
Score	6714	6714	6714	6714	6708	6708	6708	6708	6708	6708
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Human Her-2 protei	Her-2/neu		Human Her-2/neu po	c-er	Human breast cance	Human HER-2/neu pr	Rat HER-2/neu prot	Her-2/neu	Mouse Her-2/neu pr	acid	Mouse Her-2/neu on			Mouse Her-2/neu ex	Her-	HER-2	nen e	Her2-GM-CSF immuno	Extracellular HER-	Human Her-2/neu on	Human ErbB2 oncopr		DC8scFv-erbB2EC fu	Extracellular port	Amino acid sequenc	Human EGF receptor	Human Her-1 protei	н	Amino acid sequenc	Human epidermal gr	Human protein for	ini	ein f	ein f	
AAE24067	AAE20479	AAM51143	AAU77114	AAR39568	AAU98923	AAB21208	AAB21199	AAM51144	AAB21206	AAG62860	AAM51151	AAB21203	AAM51148	AAM51152	AAM51153	AAB21204	AAM51149	AAW19764	AAB21200	AAM51145	AAB60408	AAB61593	AAY44993	AAR08222	AAB19259	AAY50616	AAE23019	AAM50768	AAB68420	S.	AAE20483	B	2	AAE20482	
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ALIGNMENTS

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'note= "suitable For foreign epitope insertion"
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                                                        124..483
/label= Ligand_binding_domain
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579..593
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label= Transmembrane_domain
label = Cysteine_rich_domain
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with ceancers (self-proteins). e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 B-cell group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
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Matches 1243; Conservative
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                                                                                  VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE
                                                                                                                                                PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP
AYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
       VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                                                                                             DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA
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                           KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA
                                                                                                                                                                    LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA
                                                                                                                                                                                                                                                                                                                                 Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MHC; immunoregulatory; immune response; HER-2; adoptive immunotherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                                                                                                                                                                                                                                    Human tyrosine kinase-type receptor, HER-2.
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774..782
/note= "Antigenic epitope"
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N-PSDB; AAD19731.
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The invention relates to synthetic therapeutic compounds (antigenic peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides inco hose cells. The present confirm transduction of polynucleotides inco hose cells. The present of the invention are designed based on the HER-2 antigenic peptide
Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
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1255 AA

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                                                                                                           ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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| DPLNN------TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWK
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Score 6714;
Pred. No. 0;
98.1%;
98.3%;
                         Matches 1243; Conservative
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                                                                                                                      The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HEF and p185neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers.
                                                                                                                                                                                                                                                              Gaps
                                               which overexpress as antibody, comprises
                                                                                                                                                                                                                                     Length 1255;
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                                              Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid -
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                                                                                                                                                                                                                                    Score 6714; DE Pred. No. 0; 0; Mismatches
                                                                                               Example 3; Fig 4; 92pp; English
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.3%;
Matches 1243; Conservative
           WPI; 2001-061962/07.
N-PSDB; AAF24297.
                                                                                                                                                                                                            Sequence 1255 AA;
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OMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE 770
                                                                                            LESILRRETHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
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05-OCT-2000; 2000US-238327P.
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SCHWALL R.
SLIWKOWSKI M.
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                                                                                                                                                                                                                                                                                              The invention relates to treating a tumour in a mammal, where the tumour is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-mayransinoid conjugate. The method is useful for treating cancer or tumours of the breast. Ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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Best Local Similarity 98.3%; Pred. No. 0;
Matches 1243; Conservative 0; Mismatches
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/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
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; Pred. No. 0;
1; Mismatches
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Best Local Similarity 98.1%;
Matches 1241; Conservative
96WO-US01689
                                   95US-0414417
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                                                                                                                                                                                                               PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP
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                        LTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
                                                                                                                                                                                                       PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP
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                                                                                                                                                                                                                                                                                                                                                                                  cell; B cell; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                               response"
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676..1255
/note= "region which
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                                                                                                                                                                                                                                                                                                                                                                     HER-2/neu oncogene protein
                                                                                                                                                                                                                                                                                                                                Protein;
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This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a mailgnancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPLNNFNNFTVSFWLRVPKVSAS----HLEQLRSLTEILKGGVLIQRNPQLCYQDTILWK
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|-|||| DPLNN------TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWK
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                                                                                                                                                                                                                                                                          immune response
for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1255;
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                                                                                                                                                                                                                                                                      e of HER-2/neu polypeptides – for eliciting an HER-2/neu associated malignancy, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.0%; Score 6708; DB 20; 98.1%; Pred. No. 0;
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96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
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Best Local Similarity 98.1
Matches 1241; Conservative
                                                                                                             WASHINGTON
                                                                                                                                                          Disis ML;
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N-PSDB; AAX01912.
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                                                                                                                                                                                                                                                                                                                  preventing tumours
                     17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
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The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth factor differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
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(CORI-) CORIXA CORP.
(SMIK ) SMITHKLINE BEECHAM.
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                                   AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
                                                                                                                                      LTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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                                                            QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
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                                                                                                                                                                                                                                                                                                    LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid sequence of the SPLICE erbB-2 receptor protein.
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wound healing.
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                                                                                                                                                              The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                 an erbB 2 receptor protein designated SPLICE the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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Pred. No. 0;
1; Mismatches
                                                                                                                                          Claim 3; Fig 2; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                98.0%;
98.1%;
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Best Local Similarity 98.1'
Matches 1241; Conservative
                                                                                               Nucleic acid encoding
erbB-2, inhibitors of
                           Siegel PM,
(UYMC-) UNIV MCMASTER
                                                       2000-303768/26
                                                                                                                                                                                                                                                                                                                                                                     1255 AA;
                                                                     N-PSDB; AAA14812
                          Muller WJ,
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The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-erbB2).
                                                                                                                                                                                                                                                                                                                                                                                           ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                            New antigen-presenting cells, useful as vaccines for eliciting o
enhancing an immune response to HER-2/neu protein, particularly
for treating or preventing cancer, e.g. breast cancer
                                                                                                                                                                                                                                                                                           Length
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Best Local Similarity 98.1%;
Matches 1241; Conservative 1
  Hand-Zimmermann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                   LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
                                                                                                                                                                                                                                                                                                                                           DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA
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KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA
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immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
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                                                           VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE
LTSIISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cyctoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I), bound to a chuman leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino caids that have look identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (II) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimalant activities, and can be used in vaccines. (I), (II) cand (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (II) are useful for inducing cellular immune response to a tumour-associated antigen when incubated with a T lymphocyte to (I) or (II). Epitope conjucting the presence of bound T lymphocyte to (I) or (II). Epitope antigen when incubated with a T lymphocyte to (I) or (II). Epitope based vaccines may be avoided. Selected epitopes may be combined to chhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the apportunity to combine epitopes derived from the same pathoden. Epitope-based anti-tumour content response to multiple cumour-associated molecules addressing the problem of tumour cumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent invention.
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|21 DPLNN-----TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWK
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                An isolated prepared HER2/neu epitope useful in a vaccine for inducir
cellular immune responses for the prevention and treatment of cancer
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Best Local Similarity 98.1%;
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                                                                                                                                                                                                               VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE
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                      KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
                                                                                                QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
                                          KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
              CSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY
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bliferative disorder; prophylaxis; inflammation; antisense;
gene therapy; phosphorothioate backbone.
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hyperproliferative disor
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                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibite the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||
|PELNN------TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWK
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Epidermal Growth Factor receptor, Her2, is useful for treating
inflammation or to prevent infection in humans -
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Pred. No. 0;
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98.1%;
                                           15-SEP-2000; 2000US-0663834
12-SEP-2001; 2001WO-US28572
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Best Local Similarity 98.1
Matches 1241; Conservative
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14-AUG-2001; 2001WO-US41733
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                                                                                                     AYVWAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1021..1030
/note= "Naturally processed HLA-B44-restricted epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, Her-2/Neu protein, immune response; gene therapy, breast cancer, human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
                                                                                                                                       KGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMA
                                                                                                                                                          LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
                                                                                                                                                                  PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP
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                    KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
                                               LTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response. The patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and treatment of can dother compositions for the diagnosis, prevention and treatment of can dother compositions for the diagnosis, prevention and treatment of cancer. The invention is useful for stimulating and/or expanding T cells specific for human malignancies, for stimulating and/or expanding T cells specific for the far. 2/Neu polypeptide and for inhibiting the development of cancer in a cancer, the invention is useful for stimulating and to direct expression of a chire Her-2/Neu gene or gene fragments of interest, to isolate a full length gene from a suitable library, and to direct expression of a colypeptide in appropriate host cells. The composition is useful in gene therapeutic applications and for the treatment of cancer, preferably for the immunotherspay of breast cancer and other Her-2/Neu-secoiated malignancies. The invention is useful in gene therapy. The
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                                                                                                                                                                                                                                                                                                                                    Novel isolated Her-2/Neu polypeptide composition useful for t
prevention and diagnosis of cancer, preferably breast cancer
                                                                                                                                                                       Kalos
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98.1%; Pred. No. 0;
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14-AUG-2000; 2000US-225152P.
28-SEP-2000; 2000US-236428P.
21-FEB-2001; 2001US-270520P.
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Matches 1241; Conservative
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Vedvick TS;
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N-PSDB; AAD32743.
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                                                                        CSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY
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              YISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHH
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The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor constraints and that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and overexpression correlates with a poor prognosis in breast and covering in nucleic acids encoding them, viral vectors, and vaccines or proteins, nucleic acid molecules. In preferred fusion proteins or nucleic acid molecules. In preferred fusion proteins, the extracellular domain of protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein is elicited or enhanced by creamsfecting chells of an animal ex vivo with a nucleic acid and insolated concerned animal. The fusion protein is elicited or enhanced by creamsfecting cells of an animal ex vivo with a nucleic acid and isolated cancer cancer, especially breast, ovarian, colon, lung or prostence cancer cancer, especially breast, ovarian, colon, lung or prostence cancer cancer, a patient. I cells that specifically react with a Her-2/neu frequence or in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
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Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
tyrosine kinase; receptor; c-erbB2; gene therapy.
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Pred. No. 0;
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Best Local Similarity 98.17
Matches 1241; Conservative
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N-PSDB; ABA92250.
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ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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Matches 1241; Conservative
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28-SEP-2000; 2000US-0675904.
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                               DPLNNFNNFTVSFWLRVPKVSAS - - - - HLEQLRSLTEILKGGVLIQRNPQLCYQDTILWK
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The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-Zineu or a polymucleotide encoding the polypeptide. Annigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (AML), chronic lymphocytic leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-Zineu polypeptide.
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VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL
chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
Hodgkin's lymphoma; T cell therapy.
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Pred. No. 0;
1; Mismatches 9;
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120

Db 1131 LTCSPQPEYVNQPDVRPQPPSPREGPLPAAR Qy 1197 VENPEYLTPQGGAAPQPHPPPAFSPAFDNLY	RESULT 15 AAR39568 ID AAR39568 standard; Protein; 1433 AA. XX AC AAR39568; DT 07-FEB-1994 (first entry) XX	Homo sapiens. W09316185-A. 19-AUG-1993. 05-FEB-1992; 93US-083196	XX PA (CETU) CETUS ONCOLOGY CORP. PA (CREA-) CREATIVE BIOMOLECULES INC. XX PI HOUSTON LL, HUSTON JS, Oppermann H, XX DR WPI, 1993-272889/34. DR N-PSDB; AAQ46083. XX PY New single chain FV polypeptide binding PT antigen - for imaging or treating breas	Disclosure; pages 48-54; 87p; c-erbB-2 refers to a protein tumour cells. such as breast approx. 200,000 mol. wt. acipt. of about 5.3 (see AAQ46) the location of a stop codon Sequence 1433 AA;	Query Match Best Local Similarity 97.3%; Pred. No. 0 Matches 1234; Conservative 3; Mismatch Qy 1 MELAALCRWGLLIALLPPGAASTQVCTGTDM 1 MELAALCRWGLLLALLPPGAASTQVCTGTDM OV 61 ELTYLPTNASLSFLODIOEVOGYVLIAHNOV	
	HSDCIACLHFNHSGICELHCPALVTVNTDTFESMPNPEGRYT 296				GUTUWELMTEGAKPYDGIPAREIPDLLEKGERLPOPPICTID 956	GFFCPDPAPCAGGWHRHRISSSTRSGGGDLTLGLEPSEEA 1076 GFFCPDPAPCAGGWHRHRSSTRSGGGDLTLGLEFSEEA 1070 GFFCPPPAPCAGGWHRHRSSTRSGGGDTLGLEFSEEEA 1070 GLGMGAAKGLQSLPTHDPSPLQRYSEDPTVBLPSETDGYVAP 1136 GLGMGAAKGLQSLPTHDPSPLQRYSEDPTVBLPSETDGYVAP 1130 GPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA 1136 GHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQV 121 DPLNNFNNFTVSFWLRVPKVSASHLEQLRS 121 DPLNNTTPVTGASPGGLRELQDLRS 177 DIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRC 177 DIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRC 171 DIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRC 171 DIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRC	237 LPTDCCHEQCAAGCTGPKHSDCIACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYT [417 YISAMPDSLPDLSVFONLQVIRGRILHNGAYSLT 411 YISAMPDSLPDLSVFONLQVIRGRILHNGAYSLT 411 YISAMPDSLPDLSVFQNLQVIRGRILHTNRAVSDEC 477 NTHLCFVHTVPWDQLFRNPHQALLHTANRPEDEC 671 NTHLCFVHTVPWDQLFRNPHQALLHTANRPEDEC 673 CSOFLRGOECVEECRNLQGLPRAVARHCLPCH	CSQFLRGOECVEECRVLG CSQFLRGOECVEECRVLG KDPPFCVARCPSGVKPDI LTSIVSAVVGILLVVVLG LTSIISAVVGILLVVVLG LTSIISAVVGILLVVVLG	717 OMRILKETELRKVKVLGSGAFGTYYKGINIPDGENVKIPVAIKVLRENTSPKANKEILDE 711 OMRILKETELRKVKVLGSGAFGTYYKGINIPDGENVKIPVAIKVLRENTSPKANKEILDE 717 AYVMAGVGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHYRENRGRLGSQDLLNWCMQIA 718 AYVMAGVGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHYRENRGRLGSQDLLNWCMQIA 711 AYVMAGVGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHYRENRGRLGSQDLLNWCMQIA 712 AYVMAGVGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHYRENRGRLGSQDLLNWCMQIA 713 AYVMAGVGSPYVSRLLGICLTSTVQLYTQLMPYGCLLDHYRENRGRLGSQDLLNWCMQIA 714 AYVMAGVGSPYVSRLLGICLTSTVQLYTGLMPYGCLLDHYRENRGRLGSQDLLNWCMQIA 715 AYVMAGVGSPYVSRLLGICLTSTVQLYTGLMPYGCRVPIKWMA	LESILRRRFTHQSDVMSY 	1017 DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMYHRHRSSSTRSGGGDLTLGLESSEEEA 1011 DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMYHRHRSSSTRSGGGDLTLGLESSEEEA 1011 DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMYHRHRSSSTRSGGGDTLTLGLESSEEEA 1077 PRSPLAPSEGASDVFDDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP 1177 11111111111111111111111111111
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8t or ovarian cancer etc.
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                              LESILRRRFTHQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
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Search completed: July 22, 2003, 08:40:33 Job time : 43.1589 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 22, 2003, 08:25:54; Search time 23.0157 Seconds (without alignments) 5267.077 Million cell updates/sec

Title: Perfect score:

SEQ4-149-163-14 6848 1261 NELAALCRWGLLLALLPPGA......TFKGTPTAENPEYLGLDVPV 1261 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protein-tvrosine k	protein-tyrosine k	p-185 precursor -	epidermal growth f				>	kinase-related tra	epidermal growth f	_	protein-tyrogine k	protein-tyrosine k	epidermal growth f	kinase-related tra	protein-tyrosine k	protein-tyrosine k	epidermal growth f	protein let-23 [im	protein-tyrosine k	protein-tyrosine k	epidermal growth f			~	protein-tyrogine k	- 3	insulin receptor p	
SUMMARIES	ID	A24571	TVRTNU	148161	GOHUE	A53183	TVCHLV	A47253	S06142	A36223	JC4387	TVFVLV	TVYUH	S35745	GQFFE	S00727	B44776	TVFVEB	A36325	E88257	S70712	870713	A45558	A42032	A27131	S13807	S13808	T43220	INHUR	A36502
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	Query Match	98.0	86.4	86.4	46.2	45.9	45.4	43.4	39.0	35.3	4	25.8	24.9	24.1	24.0	23.9	23.7	23.7	22.4	19.0	19.0	٠	16.9	٠		11.8	11.0	10.7	10.3	10.2
	Score	6029	5918	5914.5	3164	3141	3110.5	2972.5	2674	2418.5	2341.5	1766.5	1703	1647	1642.5	1640	1623	1621	1531	1302	1302	1208	1157	1142	987.5	806.5	754.5	734	704	698.5
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insulin receptor p	insulin-like growt	insulin receptor p	insulin receptor-r	protein-tyrogine k	insulin-like growt	insulin-like growt	insulin receptor -	protein-tyrogine k	insulin receptor -	protein-tyrogine k	insulin receptor (tyrosine kinase Mp	protein-tyrosine k	protein-tyrosine k	mouse developmenta
A36080	T43212	A34157	B36502	T18534	1GHUR1	A33837	T30346	A54092	A56081	150612	S57245	S49004	505582	833596	148652
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ALIGNMENTS

RESULT 1 A24571	
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human NyAlternate names: -c-erb-B-2 protein precursor; kinase-related transforming protein C:Species: Homo sanions (man)	rotein e
*Cibate: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; I59509; I57622	
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito Nature 319, 230-234, 1986	Saito, T
A, Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A, Reference number: A24571; MUID:86118663; PMID:3003577	al growt
A;Accession: A24571 A;Molecule type: mRNA A:Bosidner: 1=15E5 /vww.	
A; COOBS references GB: X03363; NID: g31197; PIDN: CAA27060.1; PID: g31198 A; Semba K: Kamata N: Tovoshima K: Yamamoro T	
Proc. Natl. Acad. Sci. U.S.A. 82, 647-6501, 1985 A:Title: A v-erbB-related profroncogene c-erbR-2 is distinct from the c-erbR-1/enid	a-1/enid
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⋖.	
A;kcsiduces: /3/-1031 <55M) A;Cross-references: GB:M11767; NID:q182163; PIDN:AAA35808.1; PID:q553282	
	Seeburg
A, Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chro	res chro
A; Acterence number: A44188; MUID:860/0181; PMID:29999/4 A; Accession: A44188	
A; Molecule type: DNA	
A;kesiques: 740-910 <coul> A;Cross-references: GB:M12036; NID:q183988; PIDN:AAA35978.1; PID:q183989</coul>	
A;Residues: 1-517,'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <cou2></cou2>	
A;Cross-references: GB:M11730; NID:g183986	
A;iltle: Ampiltication of a novel v-erbB-related gene in a human mammary carcinoma. A;Reference number: IS9509: MUID:85272597: PMID:999089	. пота
A;Accession: 159509	
A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA	
A; Residues: 812-909 < REX>	
A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808 R:Tal, M.: King, C.R.: Kraus, M.H.: Hilrich A. Schlessinger J. Givol	
Mol. Cell. Biol. 7, 2597-2601, 1987	
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptio A;Reference number: IS7622; MUID:87286898: PMID:3039351	criptio
A,Accession: 157622	
A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA	
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C.Specise: Rattus norvegicus (Norway rat)
C.Date: J-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C.Accession: A24562; A61204
R.Bargmann, C.1.; Hung, M.C.; Weinberg, R.A.
Nature 319, 225-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Accession: A24562
A.Molecule type: mRNA
A.Residues: 1-1260 CBAR.
B.Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, Carcinogenesis: 12, 1975-1976, 1991
A.Ritle: Direct DNA sequencing of the rat new oncogene transmembrane domain 2-thiazolyllformamide or N-methyl-N-nitrosourea.
A.Reference number: A61204; MUID:92035293; PMID:1682063
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KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
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                                                                                                            QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
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A,Residues: 637-663, V',665-702 <MAS>
A,Note: authors translated the codon GCA for residue
C,Genetics:
A,Gene: neu
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Fi.22-125/Product: protein-tyrosine kinase erbb2 #status predicted <MAT>
Fi.22-125/Product: protein-tyrosine kinase erbb2 #status predicted <EXT>
Fi.22-125/Product: Extracellular #status predicted <EXT>
Fi.23-105/Pomain: EGF receptor extracellular domain repeat <EEI>
Fi.39-105/Domain: EGF receptor extracellular domain repeat <EEI>
Fi.54-105/Domain: intracellular #status predicted <IMT>
Fi.64-105/Domain: intracellular #status predicted <IMT>
Fi.65-125/Pomain: protein kinase homology <KIN>
Fi.66-125/Pomain: protein kinase homology <KIN>
Fi.76-134/Rogion: protein kinase ATP-binding motif Fi.66,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted Fi.686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fi.1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
                                C,Generics:
A,Gene: GDB:ERBB2; NGL; NEU; HER-2
A,Gene: GDB:ERBB2; NGL; NEU; HER-2
A,Gross-references: GDB:120613; OMIM:164870
A,Map position: 17921.1-17921.1
A,Introns: 25/1; 75/3; 147/1; 883/3
A,Introns: 25/1; 75/3; 147/1; 883/3
A,Note: the list of introns is incomplete
C,Function:
A,Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C,Superfamily: epidermal growth factor receptor; protein kinase homology
C,Keywords: ATP; autophosphorylation; duplication; glycoprotein; phospho
                   30
 A,Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C,Comment: Amplification and overexpression of this erbB-related gene occurs in about
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Pred. No. 2.9e-266;
7; Mismatches 4;
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Matches 1240; Conservative
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